



sequence listing_ST25.txt
SEQUENCE LISTING

<110> Japan Science and Technology Agency
Kuroda, Shunichi
Tanizawa, Katsuyuki
Okajima, Toshihide
Kondo, Akihiko
Ueda, Nasakazu
Seno, Masahura

<120> THERAPEUTIC DRUG USING ANTIBODY-DISPLAYING HOLLOW PROTEIN
NANOPARTICLES AND HOLLOW PROTEIN NANOPARTICLES

<130> 12480-000067/US

<150> 10/509,249

<151> 2004-09-28

<160> 245

<170> PatentIn version 3.4

<210> 1

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> Synthesized Oligonucleotide

<400> 1

gctggtggtg gtggtggtg tggtggt

27

<210> 2

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> Synthesized Oligonucleotide

<400> 2

ctgagcctga gggctgcggc cgcctcccat gccttgctg

39

<210> 3

<211> 36

<212> DNA

<213> artificial sequence

<220>

<223> Synthesized Oligonucleotide

<400> 3

ggggacctcg gatccgag cttaccagtt ctcaca

36

<210> 4

<211> 36

<212> DNA

<213> artificial sequence

sequence listing_ST25.txt

<220>
 <223> Synthesized Oligonucleotide
 <400> 4
 gaggtcgacc agctttaacg aacgcagaat tttcga 36

<210> 5
 <211> 33
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthesized Oligonucleotide
 <400> 5
 ggccgctgga gccacccgca gttcgaaaaa ggc 33

<210> 6
 <211> 33
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthesized Oligonucleotide
 <400> 6
 ggccgccttt ttcgaactgc ggggtggctcc agc 33

<210> 7
 <211> 29
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthesized Oligonucleotide
 <400> 7
 ggggtaccat gagatctttg ttgatcttg 29

<210> 8
 <211> 28
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthesized Oligonucleotide
 <400> 8
 ggccgcggtt aaatgtatac ccaaagac 28

<210> 9
 <211> 36
 <212> DNA
 <213> artificial sequence

<220>
 <223> Synthesized Oligonucleotide

sequence listing_ST25.txt

<400> 9
gggggcggcc gcgcgcaaca cgatgaagcc gtagac 36

<210> 10
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized Oligonucleotide

<400> 10
ggttgagata aaagagcttt tggcgcggcc gccttt 36

<210> 11
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized Oligonucleotide

<400> 11
cccgcggccg cccgaggaga cggtgactga ggtccc 36

<210> 12
<211> 36
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized Oligonucleotide

<400> 12
gggggcggcc gcgatgtgca gcttcaggag tcggga 36

<210> 13
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized Oligonucleotide

<400> 13
ggggcgccg ccttttattt ccaactttgt 30

<210> 14
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Synthesized Oligonucleotide

<400> 14
ggggcgccg ccttttattt ccaactttgt 30

sequence listing_ST25.txt

<210> 15
 <211> 31
 <212> DNA
 <213> artificial sequence

 <220>
 <223> synthesized oligonucleotide

 <400> 15
 ccagttggac ggcggccgcc ctgcaccgaa c 31

 <210> 16
 <211> 31
 <212> DNA
 <213> artificial sequence

 <220>
 <223> synthesized oligonucleotide

 <400> 16
 gttcgtgca gggcggccgc cgtccaactg g 31

 <210> 17
 <211> 34
 <212> DNA
 <213> artificial sequence

 <220>
 <223> synthesized oligonucleotide

 <400> 17
 caatccagat tggggcggcc gccctgcacc gaac 34

 <210> 18
 <211> 34
 <212> DNA
 <213> artificial sequence

 <220>
 <223> synthesized oligonucleotide

 <400> 18
 gttcgtgca gggcggccgc cccaatctgg attg 34

 <210> 19
 <211> 31
 <212> DNA
 <213> artificial sequence

 <220>
 <223> synthesized oligonucleotide

 <400> 19
 ggtaggagcg ggcggccgcc ctgcaccgaa c 31

 <210> 20
 <211> 31

sequence listing_ST25.txt

<212> DNA
 <213> artificial sequence

<220>
 <223> synthesized Oligonucleotide

<400> 20
 gttcgggtgca gggcggccgc ccgctcctac c 31

<210> 21
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthesized Oligonucleotide

<400> 21
 cctcaggccg gcggccgccc tgcaccgaac 30

<210> 22
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthesized Oligonucleotide

<400> 22
 gttcgggtgca gggcggccgc cctgaggatg 30

<210> 23
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthesized Oligonucleotide

<400> 23
 gttcgggtgca gggcggccgc cctgaggatg 30

<210> 24
 <211> 31
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthesized Oligonucleotide

<400> 24
 cagagtgagg ggcggccgcc ctgcaccgaa c 31

<210> 25
 <211> 31
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

```

<220>
<223> synthesized oligonucleotide

<400> 25
gttcggtgca gggcggccgc ccctcactct g 31

<210> 26
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> synthesized oligonucleotide

<400> 26
ggtaggagcg ggcggccgca gccctcaggc 30

<210> 27
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> synthesized oligonucleotide

<400> 27
gcctgagggc tgcggccgcc cgctcctacc 30

<210> 28
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> artificial synthesized peptide sequence

<400> 28
Ser Ala Trp Arg His Pro Gln Phe Gly Gly
1 5 10

<210> 29
<211> 116
<212> PRT
<213> artificial sequence

<220>
<223> artificial synthesized peptide sequence

<400> 29
Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
1 5 10 15

Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

```

sequence listing_ST25.txt

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys
115

<210> 30
<211> 39
<212> DNA
<213> artificial synthesized peptide sequence

<220>
<223> test fused

<400> 30
gctgctgctg ctgctgctag aagaagaaga agaagaaga 39

<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence Fused Peptide

<220>
<223> 21-153 + ZZ (serotype y) sequence

<400> 31
gctgctgctg ctgctgctag aagaagaaga agaagaaga 39

<210> 32
<211> 378
<212> PRT
<213> artificial sequence

<220>
<223> protein corresponding to 21-153 + ZZ (serotype y) sequence

<400> 32

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
Page 7

sequence listing_ST25.txt

20
 25
 30
 Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
 35 40 45
 Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
 50 55 60
 Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
 65 70 75 80
 Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
 85 90 95
 Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
 100 105 110
 Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
 115 120 125
 Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
 130 135 140
 Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
 145 150 155 160
 Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
 165 170 175
 Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
 180 185 190
 Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
 195 200 205
 Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
 210 215 220
 Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
 225 230 235 240
 Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
 245 250 255
 Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
 260 265 270

sequence_listing_ST25.txt

Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
355 360 365

Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 33
<211> 1134
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R) + ZZ (serotype y) sequence

<400> 33
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 120
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac 180
caaagttaa aagatgaccc aagccaaagc gctaaccctt tagcagaagc taaaaagcta 240
aatgatgctc aggcgccgaa agtagacaac aaattcaaca agaacaaca aaacgcgttc 300
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 360
ttaaagatg acccaagcca aagcgctaac cttttagcag aagctaaaaa gctaaatgat 420
gtcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 480
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 540
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 600
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt 660
tgtcctggct atcgctggat gtgtctgcgg cgttttatca tattcctctt catcctgctg 720
ctatgcctca tcttcttggt gggtcttctg gactaccaag gtatgttgcc cgtttgcct 780

sequence listing_ST25.txt

```
ctactttccag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct      840
cgaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact      900
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc      960
cgttttctct ggctcagttt actagtgccca tttgttcagt ggttcgtagg gctttccccc     1020
actgtttggc tttcagttat atggatgatg tggatttggg ggccaagtct gtacaacatc     1080
ttgagtcctt ttttacctct attaccaatt ttcttttgtc tttgggtata catt           1134
```

<210> 34

<211> 378

<212> PRT

<213> artificial sequence

<220>

<223> Protein corresponding to 21-153 (Q129R) + ZZ (serotype y)
sequence

<400> 34

```
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1          5          10          15
```

```
His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20          25          30
```

```
Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35          40          45
```

```
Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
50          55          60
```

```
Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
65          70          75          80
```

```
Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
85          90          95
```

```
Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
100         105         110
```

```
Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
115         120         125
```

```
Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
130         135         140
```

```
Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145         150         155         160
```

sequence listing_ST25.txt

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
165 170 175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
180 185 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
195 200 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
210 215 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225 230 235 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
245 250 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
260 265 270

Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
355 360 365

Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 35
<211> 1134
<212> DNA
<213> artificial sequence

<220>

sequence listing_ST25.txt

<223> 21-153 (G145R) + ZZ (serotype y) sequence

<400> 35

```
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac    60
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac    120
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgcttcatc    180
caaagttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta    240
aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc    300
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt    360
ttaaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat    420
gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc    480
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata    540
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt    600
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt    660
tgtcctggct atcgttggat gtgtctgcgg cgttttatca tattcctctt catcctgctg    720
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct    780
ctacttccag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct    840
caaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacag aaactgcact    900
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc    960
cgtttctcct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttcccc    1020
actgtttggc tttcagttat atggatgatg tgggtattggg ggccaagtct gtacaacatc    1080
ttgagtcctt tttacctct attaccaatt ttcttttgtc tttgggtata catt        1134
```

<210> 36

<211> 378

<212> PRT

<213> artificial sequence

<220>

<223> Protein corresponding to 21-153 (G145R) + ZZ (serotype y) sequence

<400> 36

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

sequence listing_ST25.txt

```

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
 50          55          60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
65          70          75          80

Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
      85          90          95

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
      100        105        110

Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
      115        120        125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
      130        135        140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145          150        155        160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
      165        170        175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
      180        185        190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
      195        200        205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
      210        215        220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225          230        235        240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
      245        250        255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
      260        265        270

Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser
      275        280        285

Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile

```

sequence listing_ST25.txt

290

295

300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
355 360 365

Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 37

<211> 1134

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 (Q129R/G145R) + ZZ-tag (serotype y) sequence

<400> 37

atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac	60
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac	120
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac	180
caaagttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaagcta	240
aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc	300
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt	360
ttaaaagatg acccaagcca aagcgtaac ctttttagcag aagctaaaaa gctaaatgat	420
gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc	480
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata	540
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt	600
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt	660
tgtcctggct atcgctggat gtgtctgcgg cgttttatca tttcctctt catcctgctg	720
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgctc	780
ctacttcag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct	840
cgaggaacct ctatgtttcc ctcttggtgc tgtacaaaac cttcggacag aaactgcact	900
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc	960

sequence listing_ST25.txt

cgtttctcct ggctcagttt actagtgccca ttgtttcagt ggttcgtagg gctttccccc 1020
actgtttggc tttcagttat atggatgatg tggatttggg ggccaagtct gtacaacatc 1080
ttgagtcctt ttttacctct attaccaatt ttcttttgtc tttgggtata catt 1134

<210> 38
<211> 378
<212> PRT
<213> artificial sequence

<220>
<223> Protein corresponding to 21-153 (Q129R/G145R) + ZZ-tag (serotype y) sequence

<400> 38

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
50 55 60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
65 70 75 80

Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
85 90 95

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
100 105 110

Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
115 120 125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
130 135 140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145 150 155 160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
165 170 175

sequence listing_ST25.txt

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
180 185 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
195 200 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
210 215 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225 230 235 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
245 250 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
260 265 270

Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser
275 280 285

Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile
290 295 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305 310 315 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
325 330 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
340 345 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
355 360 365

Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
370 375

<210> 39
<211> 933
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 + EGF (serotype y) sequence

<400> 39
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac

60

sequence listing_ST25.txt

```

ggcgggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 120
gatggcggtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaaactgcg taaggcggcc 240
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 300
caggcgggggt ttttcttggt gacaagaatc ctcaacaatac cacagagtct agactcgtgg 360
tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 540
gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 600
accagcacgg ggccatgcaa gacctgcacg attcctgtc aaggaacctc tatgtttccc 660
tcttggtgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc 720
tgggctttcg caagattcct atgggagtg gcctcagtcc gtttctcctg gctcagttta 780
ctagtccat ttgttcagt gttcgtagg ctttcccca ctgtttggct ttcagttata 840
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 900
ttaccaattt tcttttgtct ttgggtatac att 933

```

<210> 40

<211> 311

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 + EGF (serotype y) sequence

<400> 40

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20 25 30

Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35 40 45

Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50 55 60

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65 70 75 80

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85 90 95

sequence listing_ST25.txt

```

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
      100      105      110

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
      115      120      125

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
      130      135      140

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
      145      150      155      160

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
      165      170      175

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
      180      185      190

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
      195      200      205

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
      210      215      220

Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
      225      230      235      240

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
      245      250      255

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
      260      265      270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
      275      280      285

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
      290      295      300

Phe Cys Leu Trp Val Tyr Ile
      305      310

```

```

<210> 41
<211> 933
<212> DNA
<213> artificial sequence

```

sequence listing_ST25.txt

<220>

<223> 21-153 (Q129R) + EGF (serotype y) sequence

<400> 41

```
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac    60
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat    120
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt    180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggt gggaactgcg taaggcggcc    240
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta    300
caggcggggg ttttcttggt gacaagaatc ctcaacaata cacagagtct agactcgtgg    360
tggacttctc tcaatcttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc    420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg    480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg    540
gttcttctgg actaccaagg tatgttgccc gtttgtcctc tacttccagg aacatcaacc    600
accagcacgg ggccatgcaa gacctgcacg attcctgctc gaggaacctc tatgtttccc    660
tcttgttgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc    720
tgggctttcg caagattcct atgggagtg gacctcagtc gtttctcctg gctcagttta    780
ctagtccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggct ttcagttata    840
tggatgatgt ggtattgggg gccaaagtct tacaacatct tgagtcctt tttacctcta    900
ttaccaattt tcttttgtct ttgggtatac att                                933
```

<210> 42

<211> 311

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (Q129R) + EGF (serotype y) sequence

<400> 42

```
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15
```

```
His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20           25           30
```

```
Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35           40           45
```

```
Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50           55           60
```

sequence listing_ST25.txt

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
 65 70 75 80
 Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
 85 90 95
 Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
 100 105 110
 Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
 115 120 125
 Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
 130 135 140
 His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
 145 150 155 160
 Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
 165 170 175
 Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
 180 185 190
 Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
 195 200 205
 Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
 210 215 220
 Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
 225 230 235 240
 Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
 245 250 255
 Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
 260 265 270
 Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
 275 280 285
 Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
 290 295 300
 Phe Cys Leu Trp Val Tyr Ile
 305 310

sequence listing_ST25.txt

<210> 43
 <211> 933
 <212> DNA
 <213> artificial sequence

<220>
 <223> 21-153 (G145R) + EGF (serotype y) sequence

<400> 43
 atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
 ggcgccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 120
 gatggcgat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 180
 tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcy taaggcggcc 240
 gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgcta 300
 caggcggggg ttttcttggt gacaagaatc ctcaacaata cacagagtct agactcgtgg 360
 tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 420
 ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 480
 tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 540
 gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 600
 accagcacgg ggccatgcaa gacctgcacg attcctgctc aaggaacctc tatgtttccc 660
 tcttggtgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 720
 tgggctttcg caagattcct atgggagtg gctcagtc gtttctcctg gctcagttta 780
 ctagtgccat ttgttcagt gttcgtaggg ctttcccca ctgtttggct ttcagttata 840
 tggatgatgt ggtattgggg gccaaagtct tacaacatct tgagtcctt tttacctcta 900
 ttaccaattt tcttttctt ttgggtatac att 933

<210> 44
 <211> 311
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 21-153 (G145R) + EGF (serotype y) sequence

<400> 44

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
 20 25 30

sequence listing_ST25.txt

Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35 40 45

Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50 55 60

Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65 70 75 80

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85 90 95

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
100 105 110

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
115 120 125

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
130 135 140

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
145 150 155 160

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
165 170 175

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
180 185 190

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
195 200 205

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
210 215 220

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
225 230 235 240

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
245 250 255

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
260 265 270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
275 280 285

sequence listing_ST25.txt

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
290 295 300

Phe Cys Leu Trp Val Tyr Ile
305 310

<210> 45
<211> 933
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 45
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 120
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tggtgtaggt 180
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 240
gcccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 300
caggcggggg ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 360
tggaattctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 420
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 480
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 540
gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 600
accagcacgg ggccatgcaa gacctgcacg attcctgtc gaggaacctc tatgtttccc 660
tcttggtgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 720
tgggctttcg caagattcct atgggagtg gctcagtcg gtttctcctg gctcagttta 780
ctagtgccat ttgttcagt gttcgtagg ctttcccca ctgtttggct ttcagttata 840
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 900
ttaccaattt tcttttgtct ttgggtatac att 933

<210> 46
<211> 311
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 46

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
Page 23

sequence listing_ST25.txt

```

1              5              10              15
His Gln Leu Asp Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu
20              25              30
Ser His Asp Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
35              40              45
Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu
50              55              60
Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala
65              70              75              80
Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
85              90              95
Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
100             105             110
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
115             120             125
Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
130             135             140
His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
145             150             155             160
Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
165             170             175
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
180             185             190
Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
195             200             205
Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
210             215             220
Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
225             230             235             240
Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
245             250             255

```

sequence listing_ST25.txt

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
260 265 270

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
275 280 285

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
290 295 300

Phe Cys Leu Trp Val Tyr Ile
305 310

<210> 47

<211> 792

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 + STR-tag (streptavidin) (serotype y) sequence

<400> 47

atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac	60
ggcgccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag	120
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttggtg	180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta	240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcac caacctccaa tcaactacca	300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata	360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt	420
atgttgcccc tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag	480
acctgcacga ttcctgctca aggaacctct atgtttccct cttgttgctg tacaaaacct	540
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta	600
tgggagtggg cctcagtcctg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg	660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg	720
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt	780
tggtataca tt	792

<210> 48

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 + STR-tag (streptavidin) (serotype y) sequence

sequence listing_ST25.txt

<400> 48

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1      5      10      15
His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20     25     30
Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35     40     45
Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50     55     60
Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65     70     75     80
Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85     90     95
Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100    105    110
Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115    120    125
Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130    135    140
Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145    150    155    160
Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys
165    170    175
Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser
180    185    190
Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195    200    205
Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210    215    220
Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225    230    235    240

```

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 49
<211> 792
<212> DNA
<213> artificial sequence

<220>
<223> 21-153 (Q129R) + STR (serotype y) sequence

<400> 49
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 120
aacacaacat caggattcct aggacccttg ctcgtgttac aggcgggggtt tttcttgttg 180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcct caacctcaa tcactcacca 300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 420
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 480
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg taaaaaacct 540
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 600
tgggagtggg cctcagtcctg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 720
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 780
tggtataca tt 792

<210> 50
<211> 264
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 21-153 (Q129R) + STR (serotype y) sequence

<400> 50

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20 25 30

sequence listing_ST25.txt

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35 40 45

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50 55 60

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65 70 75 80

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85 90 95

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100 105 110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 51
<211> 792

sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 (G145R) + STR (serotype y) sequence

<400> 51

```
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac      60
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag      120
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttgttg      180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta      240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcct caacctcaa tcactcacca      300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata      360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt      420
atgttgcccc tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag      480
acctgcacga ttcctgctca aggaacctct atgtttcctt cttgttgctg tacaaaacct      540
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta      600
tgggagtggg cctcagtccg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg      660
ttcgtagggc tttccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg      720
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt      780
tgggtataca tt                                                    792
```

<210> 52

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (G145R) + STR (serotype y) sequence

<400> 52

```
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
20          25          30

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
35          40          45

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50          55          60
```

sequence listing_ST25.txt

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65 70 75 80

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
85 90 95

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp
100 105 110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 53

<211> 792

<212> DNA

<213> artificial sequence

<220>

<223> 21-153 (Q129R/G145R)/STR-tag (serotype y) sequence

<400> 53

atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac

60

sequence listing_ST25.txt

```

ggcgggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 120
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttggtg 180
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 240
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca 300
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 360
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 420
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 480
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 540
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 600
tgggagtggg cctcagtcg tttctcctgg ctcatgttac tagtgccatt tgttcagtgg 660
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 720
ccaagtctgt acaacatctt gagtcctttt ttacctctat taccaatttt cttttgtctt 780
tggtataca tt 792

```

<210> 54

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 21-153 (Q129R/G145R)/STR-tag (serotype y) sequence

<400> 54

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala
          20           25           30

```

```

Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly
          35           40           45

```

```

Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu
50           55           60

```

```

Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu
65           70           75           80

```

```

Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser
          85           90           95

```

```

Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp

```

sequence listing_ST25.txt

100

105

110

Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys
115 120 125

Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val
130 135 140

Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys
145 150 155 160

Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys
165 170 175

Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser
180 185 190

Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe
195 200 205

Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu
210 215 220

Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly
225 230 235 240

Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile
245 250 255

Phe Phe Cys Leu Trp Val Tyr Ile
260

<210> 55

<211> 1170

<212> DNA

<213> artificial sequence

<220>

<223> 33-153 + ZZ (serotype y) sequence

<400> 55

atgggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60

cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120

gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180

cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgaccaaacg 240

caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300

gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca tttacctaac 360

sequence listing_ST25.txt

```

ttaaacgaag aacaacgaaa cgccttcac caaagtttaa aagatgaccc aagccaaagc   420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc   480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccttgct cgtgttacag   540
gcgggggtttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg   600
acttctctca attttctagg gggagcacc cagtgctctg gccaaaattc gcagtcccca   660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt   720
ctgcggcggtt ttatcatatt cctcttcac ctagtgctat gcctcatctt cttgttggtt   780
cttctggact accaaggtat gttgcccgtt tgtcctctac ttccaggaac atcaaccacc   840
agcacggggc catgcaagac ctgcacgatt cctgctcaag gaacctctat gtttccctct   900
tgttgctgta caaaccttc ggacggaaac tgcacttgta ttcccatccc atcatcctgg   960
gctttcgcaa gattcctatg ggagtgggcc tcagtccgtt tctcctggct cagtttacta  1020
gtgccatttg ttcagtgggt cgtagggctt tccccactg tttggctttc agttatatgg  1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta  1140
ccaattttct tttgtctttg ggtatacatt  1170

```

<210> 56

<211> 390

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 + ZZ (serotype y) sequence

<400> 56

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20          25          30

```

```

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35          40          45

```

```

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50          55          60

```

```

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65          70          75          80

```

```

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
85          90          95

```

sequence_listing_ST25.txt

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100 105 110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130 135 140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145 150 155 160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165 170 175

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180 185 190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195 200 205

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

sequence_listing_ST25.txt

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 57
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R) + ZZ (serotype y) sequence

<400> 57
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120
gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca ttacctaac 360
ttaaacgaag aacaacgaaa cgccttcac caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccttgct cgtgttacag 540
gcgggggttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc acgtgtcctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt 720
ctgcggcggt ttatcatatt cctcttcac ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccgtt tgtcctctac ttccaggaac atcaaccacc 840
agcacggggc catgcaagac ctgcacgatt cctgctcgag gaacctctat gtttccctct 900
tgttgctgta caaaccttc ggacggaaac tgcacttgta ttcccatccc atcatcctgg 960
gctttcgcaa gattcctatg ggagtgggccc tcagtccgtt tctcctggct cagtttacta 1020
gtgccatttg ttcagtgggt cgtagggtt tccccactg tttggctttc agttatatgg 1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

sequence listing_ST25.txt

```

<210> 58
<211> 390
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R) + ZZ (serotype y)
sequence

<400> 58
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35 40 45

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50 55 60

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65 70 75 80

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
85 90 95

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100 105 110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130 135 140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145 150 155 160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165 170 175

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180 185 190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195 200 205

```


sequence listing_ST25.txt

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 59
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + ZZ (serotype y) sequence

<400> 59
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60

cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120

gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
Page 37

sequence listing_ST25.txt

```

cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca tttaacctaac 360
ttaaacgaag aacaacgaaa cgccttcatt caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccctgct cgtgttacag 540
gcgggggtttt tcttggtgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc cagtgctctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgctct ccaatttgct ctggctatcg ctggatgtgt 720
ctgcggcggtt ttatcatatt cctcttcatt ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccggt tgtcctctac ttccaggaac atcaaccacc 840
agcacggggc catgcaagac ctgcacgatt cctgctcaag gaacctctat gtttccctct 900
tgttgctgta caaaccttc ggacagaaac tgcacttgta ttcccatccc atcatcctgg 960
gctttcgcaa gattcctatg ggagtgggcc tcagtccggt tctcctggct cagtttacta 1020
gtgccatttg ttcagtgggt cgtagggctt tccccactg tttggctttc agttatatgg 1080
atgatgtggt attggggggc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

```

<210> 60

<211> 390

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (G145R) + ZZ (serotype y)
sequence

<400> 60

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
          20           25           30

```

```

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
          35           40           45

```

```

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50           55           60

```

sequence listing_ST25.txt

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
 65 70 75 80
 Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
 85 90 95
 Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
 100 105 110
 Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
 115 120 125
 Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
 130 135 140
 Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
 145 150 155 160
 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
 165 170 175
 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
 180 185 190
 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
 195 200 205
 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
 210 215 220
 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
 225 230 235 240
 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
 245 250 255
 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
 260 265 270
 Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
 275 280 285
 Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
 290 295 300
 Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
 305 310 315 320

sequence listing_ST25.txt

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 61
<211> 1170
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R/G145R) + ZZ (serotype y) sequence

<400> 61
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcgcgca acacgatgaa 120
gccgtagaca acaaattcaa caaagaacaa caaaacgcgt tctatgagat cttacattta 180
cctaacttaa acgaagaaca acgaaacgcc ttcattccaaa gtttaaaaga tgacccaagc 240
caaagcgcta accttttagc agaagctaaa aagctaaatg atgctcaggc gccgaaagta 300
gacaacaaat tcaacaaaga acaacaaaac gcgttctatg agatcttaca tttacctaac 360
ttaaacgaag aacaacgaaa cgccttcatt caaagtttaa aagatgaccc aagccaaagc 420
gctaaccttt tagcagaagc taaaaagcta aatgatgctc aggcgccgaa agcggccgcc 480
cctgcaccga acatggagaa cacaacatca ggattcctag gacccctgct cgtgttacag 540
gcgggggttt tcttgttgac aagaatcctc acaataccac agagtctaga ctcgtggtgg 600
acttctctca attttctagg gggagcacc acgtgtcctg gccaaaattc gcagtcccca 660
acctccaatc actcaccaac ctcttgcctt ccaatttgct ctggctatcg ctggatgtgt 720
ctgcggcggt ttatcatatt cctcttcatt ctgctgctat gcctcatctt cttgttggtt 780
cttctggact accaaggtat gttgcccggt tgtcctctac ttccaggaac atcaaccacc 840
agcacggggc catgcaagac ctgcacgatt cctgctcgag gaacctctat gtttccctct 900
tgttgctgta caaaccttc ggacagaaac tgcacttgta ttcccatccc atcatcctgg 960
gctttcgcaa gattcctatg ggagtgggccc tcagtccggt tctcctggct cagtttacta 1020

sequence listing_ST25.txt

gtgccatttg ttcagtgggt cgtagggcct tccccactg tttggctttc agttatatgg 1080
atgatgtggg attgggggcc aagtctgtac aacatcttga gtcccttttt acctctatta 1140
ccaattttct tttgtctttg ggtatacatt 1170

<210> 62
<211> 390
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R/G145R) + ZZ (serotype y)
sequence

<400> 62

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys
35 40 45

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn
50 55 60

Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
65 70 75 80

Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
85 90 95

Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
100 105 110

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu
130 135 140

Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala
145 150 155 160

Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
165 170 175

sequence_listing_ST25.txt

Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
180 185 190

Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
195 200 205

Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
210 215 220

Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
225 230 235 240

Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
245 250 255

Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
260 265 270

Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
275 280 285

Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
290 295 300

Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
305 310 315 320

Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
325 330 335

Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
340 345 350

Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
355 360 365

Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
370 375 380

Cys Leu Trp Val Tyr Ile
385 390

<210> 63

<211> 969

<212> DNA

<213> artificial sequence

<220>

<223> 33-153 + EGF (serotype y) sequence

sequence listing_ST25.txt

```

<400> 63
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac      60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc      120
gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgtatgcat gtacatcgaa      180
gctctggaca aatacgcgat caactgtgtt gtaggttaca tcggcgaacg ttgccagtat      240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagAAC      300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca      360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg      420
ggagcaccca cgtgtcctgg ccaaaattcg cagtcccca cctccaatca ctcaccaacc      480
tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc      540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggatg      600
ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc      660
tgcacgattc ctgctcaagg aacctctatg tttccctctt gttgctgtac aaaaccttcg      720
gacggaaact gcacttgat tcccatccca tcactctggg ctttcgcaag attcctatgg      780
gagtgggcct cagtccgttt ctcctggctc agtttactag tgccatttgt tcagtgggtc      840
gtagggcttt cccctactgt ttggctttca gttatatgga tgatgtggta ttgggggcca      900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg      960
gtatacatt
969

```

```

<210> 64
<211> 323
<212> PRT
<213> artificial sequence

```

```

<220>
<223> Proteins corresponding to 33-153 + EGF (serotype y). sequence

```

```

<400> 64

```

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10          15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20          25          30

```

```

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35          40          45

```

```

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50          55          60

```

sequence listing_ST25.txt

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
 65 70 75 80
 Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
 85 90 95
 Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
 100 105 110
 Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
 115 120 125
 Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
 130 135 140
 Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
 145 150 155 160
 Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
 165 170 175
 Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu
 180 185 190
 Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
 195 200 205
 Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
 210 215 220
 Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
 225 230 235 240
 Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
 245 250 255
 Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
 260 265 270
 Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
 275 280 285
 Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
 290 295 300
 Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
 305 310 315 320

sequence listing_ST25.txt

Val Tyr Ile

<210> 65
<211> 969
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R) + EGF (serotype y) sequence

<400> 65
atgggggacga atcttttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc 120
gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgtatgcat gtacatcgaa 180
gctctggaca aatacgcatg caactgtggt gtaggttaca tcggcgaacg ttgccagtat 240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagaac 300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca 360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg 420
ggagcaccca cgtgtcctgg ccaaaattcg cagtcccca cctccaatca ctcaccaacc 480
tcttgcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc 540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggtagt 600
ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc 660
tgcacgattc ctgctcgagg aacctctatg tttccctctt gttgctgtac aaaaccttcg 720
gacggaaact gcacttgat tcccatccca tcatcctggg ctttcgcaag attcctatgg 780
gagtgggcct cagtccgttt ctcttggtc agtttactag tgccatttgt tcagtgggtc 840
gtagggttt cccctactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
gtatacatt 969

<210> 66
<211> 323
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R) + EGF (serotype y) sequence

<400> 66

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

sequence listing_ST25.txt

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
210 215 220

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

sequence listing_ST25.txt

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 67
<211> 969
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + EGF (serotype y) sequence

<400> 67
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc 120
gaatgcccgc tgtctcatga cggttactgc ctgcatgatg gcgatgcat gtacatcgaa 180
gctctggaca aatacgcgat caactgtgtt gtaggttaca tcggcgaacg ttgccagtat 240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagaac 300
acaacatcag gattcctagg acccctgctc gtgttacagg cggggttttt cttgttgaca 360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg 420
ggagcaccca cgtgtcctgg ccaaaattcg cagtcccaa cctccaatca ctcaccaacc 480
tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc 540
ctcttcatcc tgctgctatg ctcattcttc ttgttggttc ttctggacta ccaaggtatg 600
ttgcccgttt gtccttact tccaggaaca tcaaccacca gcacggggcc atgcaagacc 660
tgcacgattc ctgctcaagg aacctctatg tttccctctt gttgctgtac aaaaccttcg 720
gacagaaact gcacttgat tcccatccca tcattcctggg ctttcgcaag attcctatgg 780
gagtgggcct cagtccgttt ctctggctc agtttactag tgccatttgt tcagtggttc 840
gtagggcttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
gtatacatt 969

<210> 68

sequence listing_ST25.txt

<211> 323

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (G145R) + EGF (serotype y)
sequence

<400> 68

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro

sequence listing_ST25.txt

210

215

220

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 69
<211> 969
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 69
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgcatgaa ctctgattcc 120
gaatgcccg cgtctcatga cggttactgc ctgcatgatg gcgtatgcat gtacatcgaa 180
gctctggaca aatacgcgat caactgtgtt gtaggttaca tcggcgaacg ttgccagtat 240
cgcgacctga aatggtggga actgcgtaag gcggccgccc ctgcaccgaa catggagAAC 300
acaacatcag gattcctagg acccctgctc gtgttacagg cgggggtttt cttgttgaca 360
agaatcctca caataccaca gagtctagac tcgtggtgga cttctctcaa ttttctaggg 420
ggagcaccga cgtgtcctgg ccaaaattcg cagtcccca cctccaatca ctcaccaacc 480
tcttgtcctc caatttgtcc tggctatcgc tggatgtgtc tgcggcgttt tatcatattc 540
ctcttcatcc tgctgctatg cctcatcttc ttgttggttc ttctggacta ccaaggatatg 600
ttgcccgttt gtcctctact tccaggaaca tcaaccacca gcacggggcc atgcaagacc 660
tgcacgattc ctgctcgagg aacctctatg tttccctctt gttgctgtac aaaaccttcg 720

sequence listing_ST25.txt

gacagaaact gcacttgat tcccatccca tcctcctggg ctttcgcaag attcctatgg 780
gagtgggcct cagtcggtt ctcttggtc agtttactag tgccatttgt tcagtgggtc 840
gtagggcttt cccccactgt ttggctttca gttatatgga tgatgtggta ttgggggcca 900
agtctgtaca acatcttgag tcccttttta cctctattac caattttctt ttgtctttgg 960
gtatacatt 969

<210> 70
<211> 323
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 33-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 70

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
35 40 45

Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys
50 55 60

Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr
65 70 75 80

Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro
85 90 95

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
100 105 110

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
115 120 125

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
130 135 140

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
145 150 155 160

sequence listing_ST25.txt

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
165 170 175

Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu
180 185 190

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
195 200 205

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
210 215 220

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
225 230 235 240

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
245 250 255

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
260 265 270

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
275 280 285

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
290 295 300

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
305 310 315 320

Val Tyr Ile

<210> 71
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 + STR-tag (serotype y) sequence

<400> 71
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat tttctagggg gagcaccac gtgtcctggc 300

sequence listing_ST25.txt

```

caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcacct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggatatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcaagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acggaaactg cacttgattt 600
cccatcccat catcctgggc ttctgcaaga ttctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactggt 720
tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780
ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

```

<210> 72

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 + STR-tag (serotype y) sequence

<400> 72

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

sequence listing_ST25.txt

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 73
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R) + STR-tag (serotype y) sequence

<400> 73
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat tttctagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcacct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggtatgt tgcccgtttg tcctctactt 480

sequence listing_ST25.txt

ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcgagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acggaaactg cacttgatt 600
cccatcccat catcctgggc tttcgcaaga ttcctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactgtt 720
tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780
ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

<210> 74

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (Q129R) + STR-tag (serotype y)
sequence

<400> 74

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

sequence listing_ST25.txt

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 75
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (G145R) + STR-tag (serotype y) sequence

<400> 75
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat tttctagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgtcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcatcct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggatatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcaagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acagaaactg cacttgtatt 600
cccatcccat catcctgggc tttcgcaaga ttcctatggg agtgggcctc agtccgtttc 660

sequence listing_ST25.txt

tcctggctca gtttactagt gccatttggt cagtgggtcg tagggctttc cccactggt 720
 tggctttcag ttatatggat gatgtggtat tgggggccaa gtctgtacaa catcttgagt 780
 ccctttttac ctctattacc aattttcttt tgtctttggg tatacatt 828

<210> 76

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (G145R) + STR-tag (serotype y)
 sequence

<400> 76

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
 35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
 50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
 85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
 100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
 115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
 130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
 145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
 165 170 175

sequence listing_ST25.txt

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
195 200 205

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 77
<211> 828
<212> DNA
<213> artificial sequence

<220>
<223> 33-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 77
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattggggcg gccgctggag ccacccgcag 120
ttcgaaaaag cggccgcccc tgcaccgaac atggagaaca caacatcagg attcctagga 180
cccctgctcg tgttacaggc ggggtttttc ttgttgacaa gaatcctcac aataccacag 240
agtctagact cgtggtggac ttctctcaat tttctagggg gagcaccac gtgtcctggc 300
caaaattcgc agtccccaac ctccaatcac tcaccaacct cttgtcctcc aatttgcct 360
ggctatcgct ggatgtgtct gcggcgtttt atcatattcc tcttcatcct gctgctatgc 420
ctcatcttct tgttggttct tctggactac caaggtatgt tgcccgtttg tcctctactt 480
ccaggaacat caaccaccag cacggggcca tgcaagacct gcacgattcc tgctcgagga 540
acctctatgt ttccctcttg ttgctgtaca aaaccttcgg acagaaactg cacttgatt 600
cccatcccat catcctgggc ttctgcaaga ttcctatggg agtgggcctc agtccgtttc 660
tcctggctca gtttactagt gccatttggt cagtggttcg tagggctttc cccactggt 720
tggctttcag ttatatggat gatgtggtat tgggggcca gtctgtacaa catcttgagt 780

cccttttttac ctctattacc aattttcttt tgtctttggg tatacatt

<210> 78

<211> 276

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 33-153 (Q129R/G145R) + STR-tag
(serotype y) sequence

<400> 78

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala
35 40 45

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
50 55 60

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
65 70 75 80

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
85 90 95

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
100 105 110

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
115 120 125

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
130 135 140

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
145 150 155 160

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
165 170 175

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
180 185 190

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
Page 58

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
210 215 220

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
225 230 235 240

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
245 250 255

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
260 265 270

Trp Val Tyr Ile
275

<210> 79
<211> 1221
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 + ZZ (serotype y) sequence

<400> 79
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tgccagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac 180
aacaattca acaagaaca acaaacgcg ttctatgaga tttacattt acctaactta 240
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgaccaag ccaaagcgct 300
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
ttcaacaaag aacaacaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa 420
gaacaacgaa acgccttcat ccaaagttaa aaagatgacc caagccaaag cgtaacctt 480
ttagcagaag ctaaaaagct aaatgatgct caggcgccga aagcggccgc ccctgcaccg 540
aacatggaga acacaacatc aggattccta ggaccctcgc tcgtgttaca ggcgggggtt 600
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 720
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac 840
taccaaggta tgttgcccggt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
ccatgcaaga cctgcacgat tcctgtctca ggaacctcta tgtttcctc ttgttgctgt 960

sequence listing_ST25.txt

acaaaacctt cggacggaaa ctgcacttgt attcccatcc catcatcctg ggcttttcgca 1020
 agattcctat gggagtgggc ctcagtcctgt ttctcctggc tcagtttact agtgccattt 1080
 gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 1140
 tattgggggc caagtctgta caacatcttg agtcctttt tacctctatt accaattttc 1200
 ttttgccttt gggatacat t 1221

<210> 80
 <211> 407
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 + ZZ (serotype y) sequence
 <400> 80

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
 50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
 65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
 85 90 95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
 100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
 145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
 Page 60

sequence_listing_ST25.txt

```

165                                     170                                     175
Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
180                                     185                                     190
Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195                                     200                                     205
Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210                                     215                                     220
Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225                                     230                                     235
His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245                                     250                                     255
Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260                                     265                                     270
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275                                     280                                     285
Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290                                     295                                     300
Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305                                     310                                     315                                     320
Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325                                     330                                     335
Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340                                     345                                     350
Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355                                     360                                     365
Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370                                     375                                     380
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385                                     390                                     395                                     400
Phe Cys Leu Trp Val Tyr Ile
405

```

sequence listing_ST25.txt

<210> 81
 <211> 1221
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (Q129R) + ZZ (serotype y) sequence

<400> 81
 atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
 cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
 tggccagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac 180
 aacaaattca acaaaagaaca acaaaacgcg ttctatgaga tcttacattt acctaactta 240
 aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 300
 aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
 ttcaacaaag aacaacaaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa 420
 gaacaacgaa acgccttcat ccaaagttta aaagatgacc caagccaaag cgctaacctt 480
 ttagcagaag ctaaaaagct aaatgatgct caggcgccga aagcggccgc ccctgcaccg 540
 aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 600
 ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
 aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 720
 cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
 tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac 840
 taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
 ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttggtgctgt 960
 acaaaacctt cggacggaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca 1020
 agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 1080
 gttcagtggt tcgtagggct ttccccact gtttggtgtt cagttatatg gatgatgtgg 1140
 tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 1200
 ttttgtcttt gggatacat t 1221

<210> 82
 <211> 407
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (Q129R) + ZZ (serotype y) sequence

<400> 82

sequence listing_ST25.txt

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1      5      10      15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
      20      25      30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
      35      40      45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
      50      55      60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
      65      70      75      80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
      85      90      95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
      100      105      110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
      115      120      125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
      130      135      140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
      145      150      155      160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
      165      170      175

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
      180      185      190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
      195      200      205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
      210      215      220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
      225      230      235      240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
      245      250      255

```

sequence_listing_ST25.txt

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340 345 350

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 83

<211> 1221

<212> DNA

<213> artificial sequence

<220>

<223> 50-153 (G145R) + ZZ (serotype y) sequence

<400> 83

atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac	60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa	120
tggccagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac	180
aacaaattca acaaagaaca acaaaacgcg ttctatgaga ttttacattt acctaactta	240
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct	300
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa	360
ttcaacaaag aacaacaaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa	420

sequence listing_ST25.txt

```

gaacaacgaa acgccttcat ccaaagttta aaagatgacc caagccaaag cgtaacctt 480
ttagcagaag ctaaaaagct aaatgatgct caggcgccga aagcggccgc ccctgcaccg 540
aacatggaga acacaacatc aggattccta ggaccctgc tcgtgttaca ggcgggggtt 600
ttcttgttga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcctc aacctccaat 720
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac 840
taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
ccatgcaaga cctgcacgat tcctgctcaa ggaacctcta tgtttcctc ttgttgctgt 960
acaaaacctt cggacagaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca 1020
agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 1080
gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 1140
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 1200
ttttgtcttt gggatacat t 1221

```

<210> 84
 <211> 407
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (G145R) + ZZ (serotype y)
 sequence

<400> 84

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
 50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
 65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
 85 90 95

sequence listing_ST25.txt

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
165 170 175

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
180 185 190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195 200 205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210 215 220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225 230 235 240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245 250 255

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser

sequence listing_ST25.txt
345 350

340

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 85
<211> 1221
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + ZZ (serotype y) sequence

<400> 85
atgggggacga atcttttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcggttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tgccagagg caaatcaggt aggagcgggc ggccgcgcgc aacacgatga agccgtagac 180
aacaattca acaaagaaca aaaaacgcg ttctatgaga tttacattt acctaactta 240
aacgaagaac aacgaaacgc cttcatcaa agtttaaaag atgacccaag ccaaagcgct 300
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagt agacaacaaa 360
ttcaacaaag aacaacaaaa cgcgttctat gagatcttac atttacctaa cttaaacgaa 420
gaacaacgaa acgccttcat ccaaagtta aaagatgacc caagccaaag cgctaacctt 480
ttagcagaag ctaaaagct aaatgatgct caggcgccga aagcgccgc ccctgcaccg 540
aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 600
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 660
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 720
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 780
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac 840
taccaaggta tgttgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 900
ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttgttgctgt 960
aaaaaacctt cggacagaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca 1020
agattcctat gggagtgggc ctcagtccgt ttctcctggc tcagtttact agtgccattt 1080

sequence listing_ST25.txt

gttcagtggg tcgtagggct ttccccact gtttggcttt cagttatatg gatgatgtgg 1140
tattgggggc caagtctgta caacatcttg agtcctttt tacctctatt accaattttc 1200
ttttgtcttt gggatacat t 1221

<210> 86
<211> 407
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 (Q129R/G145R) + ZZ (serotype y)
sequence

<400> 86

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

Ala Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
85 90 95

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
100 105 110

Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
115 120 125

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
130 135 140

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
145 150 155 160

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala
165 170 175

sequence listing_ST25.txt

Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro
180 185 190

Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr
195 200 205

Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly
210 215 220

Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn
225 230 235 240

His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met
245 250 255

Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
260 265 270

Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys
275 280 285

Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr
290 295 300

Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys
305 310 315 320

Thr Lys Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser
325 330 335

Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser
340 345 350

Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser
355 360 365

Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
370 375 380

Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe
385 390 395 400

Phe Cys Leu Trp Val Tyr Ile
405

<210> 87
<211> 1020
<212> DNA

sequence listing_ST25.txt

<213> artificial sequence

<220>

<223> 50-153 + EGF (serotype y) sequence

<400> 87

```

atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac      60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa      120
tgccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg      180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac      240
aaatacgcag gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg      300
aaatggtggg aactgcgtaa ggcggccgcc cctgcaccga acatggagaa cacaacatca      360
ggattcctag gacccttgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc      420
acaataccac agagtctaga ctctgtgttg acttctctca attttctagg gggagcacc      480
acgtgtcctg gccaaaattc gcagtcccca acctccaatc actcaccaac ctcttgctct      540
ccaatttgct ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac      600
ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccgtt      660
tgtcctctac ttccaggaac atcaaccacc agcacggggc catgcaagac ctgcacgatt      720
cctgctcaag gaacctctat gtttccctct tgttgctgta caaaccttc ggacggaaac      780
tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc      840
tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggcct      900
tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac      960
aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt     1020

```

<210> 88

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 + EGF (serotype y) sequence

<400> 88

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20           25           30

```

```

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35           40           45

```

sequence_listing_ST25.txt

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

sequence listing_ST25.txt

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 89
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R) + EGF (serotype y) sequence

<400> 89
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240
aaatacgcat gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatgggtggg aactgcgtaa ggcggccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gaccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc 420
acaataccac agagtctaga ctctgtgtgg acttctctca attttctagg gggagcaccc 480
acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccaac ctcttgtcct 540
ccaatttgct ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcata 600
ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggat gttgcccgtt 660
tgtcctctac ttccaggaa atcaaccacc agcacggggc catgcaagac ctgcacgatt 720
cctgctcgag gaacctctat gtttcctct tgttgctgta caaaccttc ggacggaaac 780
tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
tcagtcctgt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggctt 900
tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

<210> 90
<211> 340
<212> PRT
<213> artificial sequence

<220>

sequence listing_ST25.txt

<223> Proteins corresponding to 50-153 (Q129R) + EGF (serotype y)
sequence

<400> 90

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

sequence_listing_ST25.txt

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 91
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (G145R) + EGF (serotype y) sequence

<400> 91
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240
aaatacgcag gcaactgtgt tgtaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatgggtggg aactgcgtaa ggcgggccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gaccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc 420
acaataccac agagtctaga ctcgtggtgg acttctctca attttctagg gggagcaccc 480
acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccaac ctcttgctct 540
ccaatttgct ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 600
ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccggt 660
tgtcctctac ttccaggaac atcaaccacc agcacggggc catgcaagac ctgcacgatt 720

sequence_listing_ST25.txt

cctgctcaag gaacctctat gtttcctct tgttgctgta caaaccttc ggacagaaac 780
 tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
 tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggcct 900
 tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

<210> 92

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 (G145R) + EGF (serotype y)
 sequence

<400> 92

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
 50 55 60

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
 65 70 75 80

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
 85 90 95

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
 100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
 115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
 145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro

sequence listing_ST25.txt

165

170

175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

<210> 93
<211> 1020
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + EGF (serotype y) sequence

<400> 93
atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgcatga actctgattc cgaatgcccg 180
ctgtctcatg acggttactg cctgcatgat ggcgtatgca tgtacatcga agctctggac 240

sequence listing_ST25.txt

```

aaatacgcacat gcaactgtgt ttaggttac atcggcgaac gttgccagta tcgcgacctg 300
aaatgggtggg aactgcgtaa ggcgccgcc cctgcaccga acatggagaa cacaacatca 360
ggattcctag gacccctgct cgtgttacag gcggggtttt tcttggtgac aagaatcctc 420
acaataccac agagtctaga ctctgtgttg acttctctca attttctagg gggagcacc 480
acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccaac ctcttgctct 540
ccaatttgtc ctggctatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 600
ctgtgtctat gcctcatctt cttgttggtt cttctggact accaagggtat gttgcccggt 660
tgtcctctac ttccaggaac atcaaccacc agcacggggc catgcaagac ctgcacgatt 720
cctgtctgag gaacctctat gtttccctct tgttgctgta caaaccttc ggacagaaac 780
tgcacttgta ttcccatccc atcatcctgg gctttcgcaa gattcctatg ggagtgggcc 840
tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtgggt cgtagggtt 900
tccccactg tttggctttc agttatatgg atgatgtggt attgggggcc aagtctgtac 960
aacatcttga gtccctttt acctctatta ccaattttct tttgtctttg ggtatacatt 1020

```

<210> 94

<211> 340

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 50-153 (Q129R/G145R) + EGF (serotype y)
sequence

<400> 94

```

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1           5           10           15

```

```

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20           25           30

```

```

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35           40           45

```

```

Ala Gly Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
50           55           60

```

```

Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
65           70           75           80

```

```

Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
85           90           95

```

sequence listing_ST25.txt

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala
100 105 110

Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val
115 120 125

Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
130 135 140

Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
145 150 155 160

Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro
165 170 175

Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg
180 185 190

Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu
195 200 205

Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu
210 215 220

Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile
225 230 235 240

Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro
245 250 255

Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe
260 265 270

Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser
275 280 285

Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val
290 295 300

Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr
305 310 315 320

Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
325 330 335

Trp Val Tyr Ile
340

sequence listing_ST25.txt

<210> 95
<211> 879
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 + STR-tag (serotype y) sequence

<400> 95
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tgccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
cagtcccaa cctccaatca ctcaccaacc tcttgtcctc caatttgtcc tggctatcgc 420
tggtgtgtc tgcggcggtt tatcatattc ctcttcaccc tgctgctatg cctcatcttc 480
ttgttggttc ttctggacta ccaaggatg ttgcccgttt gtcctctact tccaggaaca 540
tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcaagg aacctctatg 600
ttccctctt gttgctgtac aaaaccttcg gacggaaact gcacttgat tcccatccca 660
tcctctggg ctttcgcaag attcctatgg gaggggcct cagtccgttt ctctggctc 720
agtttactag tgccatttgt tcagtgggtc gtagggcttt cccccactgt ttggctttca 780
gttatatgga tgatgtggtt ttgggggcca agtctgtaca acatcttgag tcccttttta 840
cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 96
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 + STR-tag (serotype y) sequence

<400> 96

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile
290

sequence listing_ST25.txt

<210> 97
 <211> 879
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (Q129R) + STR-tag (serotype y) sequence

<400> 97
 atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
 cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
 tggccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
 gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
 gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
 tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
 cagtcccaa cctccaatca ctcaccaacc tcttgtcctc caatttgtcc tggctatcgc 420
 tggatgtgtc tgcggcgttt tatcatattc ctcttcattc tgctgctatg cctcatcttc 480
 ttgttggttc ttctggacta ccaaggtatg ttgcccgttt gtcctctact tccaggaaca 540
 tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcgagg aacctctatg 600
 tttccctctt gttgctgtac aaaaccttcg gacggaaact gcacttgat tcccatccca 660
 tcatcctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcctggctc 720
 agtttactag tgccatttgt tcagtggttc gtagggcctt cccccactgt ttggccttca 780
 gttatatgga tgatgtggtt ttgggggcca agtctgtaca acatcttgag tcccttttta 840
 cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 98
 <211> 293
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (Q129R) + STR-tag (serotype y) sequence

<400> 98

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile
290

sequence listing_ST25.txt

<210> 99
 <211> 879
 <212> DNA
 <213> artificial sequence

<220>
 <223> 50-153 (G145R) + STR-tag (serotype y) sequence

<400> 99
 atggggacga atctttctgt tccaatcct ctgggattct ttcccgatca ccagttggac 60
 cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
 tggccagagg caaatcaggt aggagcgggc ggccgctgga gccaccgcga gttcgaaaaa 180
 gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
 gtgttacagg cggggttttt cttgttgaca agaatcctca caataccaca gagtctagac 300
 tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaatttcg 360
 cagtcccca cctccaatca ctaccaacc tcttgcctc caatttgtcc tggctatcgc 420
 tggatgtgtc tgcggcggtt tatcatattc ctcttcatcc tgctgctatg cctcatcttc 480
 ttgttggttc ttctggacta ccaaggtatg ttgcccggtt gtcctctact tccaggaaca 540
 tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcaagg aacctctatg 600
 tttccctctt gttgctgtac aaaaccttcg gacagaaact gcacttgtat tcccatccca 660
 tcatcctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcttggtc 720
 agtttactag tgccatttgt tcagtgggtc gtagggcttt cccccactgt ttggctttca 780
 gttatatgga tgatgtggta ttgggggcca agtctgtaca acatcttgag tcccttttta 840
 cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 100
 <211> 293
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 50-153 (G145R) + STR-tag (serotype y) sequence

<400> 100

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
 1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
 20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
 35 40 45

sequence listing_ST25.txt

Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
50 55 60

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
65 70 75 80

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
85 90 95

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
100 105 110

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
115 120 125

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
130 135 140

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
145 150 155 160

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
165 170 175

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
180 185 190

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
195 200 205

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
210 215 220

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
225 230 235 240

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
245 250 255

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
260 265 270

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
275 280 285

Leu Trp Val Tyr Ile

sequence listing_ST25.txt

290

<210> 101
<211> 879
<212> DNA
<213> artificial sequence

<220>
<223> 50-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 101
atggggacga atctttctgt tcccaatcct ctgggattct ttcccgatca ccagttggac 60
cctgcgttcg gagccaactc aaacaatcca gattgggact tcaaccccaa caaggatcaa 120
tggccagagg caaatcaggt aggagcgggc ggccgctgga gccacccgca gttcgaaaaa 180
gcggccgccc ctgcaccgaa catggagaac acaacatcag gattcctagg acccctgctc 240
gtgttacagg cgggggtttt cttgttgaca agaatcctca caataccaca gagtctagac 300
tcgtggtgga cttctctcaa ttttctaggg ggagcaccca cgtgtcctgg ccaaaattcg 360
cagtcccaa cctccaatca ctcaccaacc tcttgcctc caatttgtcc tggctatcgc 420
tggatgtgtc tgcggcggtt tatcatattc ctcttcattc tgctgctatg cctcatcttc 480
ttgttggttc ttctggacta ccaaggatat ttgcccgttt gtcctctact tccaggaaca 540
tcaaccacca gcacggggcc atgcaagacc tgcacgattc ctgctcgagg aacctctatg 600
ttccctctt gttgctgtac aaaaccttcg gacagaaact gcacttgat tcccatccca 660
tcacctggg ctttcgcaag attcctatgg gagtgggcct cagtccgttt ctcctggctc 720
agtttactag tgccatttgt tcagtggttc gtagggcttt cccccactgt ttggctttca 780
gttatatgga tgatgtggtt ttggggggcca agtctgtaca acatcttgag tcccttttta 840
cctctattac caattttctt ttgtctttgg gtatacatt 879

<210> 102
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 50-153 (Q129R/G145R) + STR-tag (serotype y) sequence

<400> 102
Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
1 5 10 15

His Gln Leu Asp Pro Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp
20 25 30

Asp Phe Asn Pro Asn Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly
Page 85

35 Ala Gly Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro
 50 55 60
 65 Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
 70 75 80
 85 Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
 90 95
 100 Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
 105 110
 115 Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
 120 125
 130 Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
 135 140
 145 Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
 150 155 160
 165 Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
 170 175
 180 Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
 185 190
 195 Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
 200 205
 210 Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
 215 220
 225 Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
 230 235 240
 245 Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
 250 255
 260 Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
 265 270
 275 Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
 280 285

sequence listing_ST25.txt

Leu Trp Val Tyr Ile
290

<210> 103
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + ZZ (serotype d; claim12) sequence

<400> 103
atgggagggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag ctaaattgatg ctgaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
gggtttttct tggtgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacg tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aagggtatgtt gcccgtttgt cctctacttc caggaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcaaggaa cctctatgtt tccctcttgt 900
tgctgtacaa aaccttcgga cggaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtgt 1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
atcttctttt gtctttgggt atacatt 1167

<210> 104
<211> 389
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 + ZZ (serotype d; claim12) sequence

sequence listing_ST25.txt

<400> 104

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10     15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20     25     30
Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
35     40     45
Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
50     55     60
Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65     70     75     80
Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
85     90     95
Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
100    105    110
Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115    120    125
Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130    135    140
Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145    150    155    160
Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165    170    175
Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180    185    190
Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195    200    205
Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210    215    220
Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225    230    235    240
Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe

```

sequence_listing_ST25.txt

245

250

255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr Ile
385

<210> 105
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R) + ZZ (serotype d) sequence

<400> 105
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag cttaatgatg ctcaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480

sequence listing_ST25.txt

```
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg      540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact      600
tctctcaatt ttctaggggg agcaccacag tgtcctggcc aaaattcgca gtccccaacc      660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg      720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt      780
ctggactacc aaggatggtt gcccgtttgt cctctacttc caggaacatc aaccaccagc      840
acggggccat gcaagacctg cacgattcct gctcgaggaa cctctatggt tccctcttgt      900
tgctgtacaa aaccttcgga cggaaactgc acttgatttc ccatcccatc atcctgggct      960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg     1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg     1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca     1140
attttctttt gtctttgggt atacatt                                     1167
```

<210> 106
 <211> 388
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (Q129R) + ZZ (serotype d)
 sequence

<400> 106

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
 35 40 45

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
 50 55 60

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
 65 70 75 80

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
 85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
 100 105 110

sequence listing_ST25.txt

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115 120 125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130 135 140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145 150 155 160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165 170 175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180 185 190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195 200 205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210 215 220

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225 230 235 240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
245 250 255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu

355

sequence listing_ST25.txt
360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr
385

<210> 107
<211> 1167
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (G145R) + ZZ (serotype d) sequence

<400> 107
atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120
gtagacaaca aattcaacaa agaacaacaa aacgcgttct atgagatctt acatttacct 180
aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240
agcgctaacc ttttagcaga agctaaaaag ctaaagtatg ctcaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaacgcg ttctatgaga tcttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacag tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aaggatgtt gcccgtttgt cctctacttc caggaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcaaggaa cctctatgtt tccctcttgt 900
tgctgtacaa aaccttcgga cagaaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg 1020
ccatttgttc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
atcttctttt gtctttgggt atacatt 1167

<210> 108
<211> 389

sequence listing_ST25.txt

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (G145R) + ZZ (serotype d)
sequence

<400> 108

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
35 40 45

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
50 55 60

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65 70 75 80

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
100 105 110

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115 120 125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130 135 140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145 150 155 160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165 170 175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180 185 190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195 200 205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210 215 220

sequence listing_ST25.txt

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225 230 235 240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe
245 250 255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr Ile
385

<210> 109

<211> 1167

<212> DNA

<213> artificial sequence

<220>

<223> 32-164 (Q129R/G145R) + ZZ-tag (serotype d) sequence

<400> 109

atgggagggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttccaat 60

cctctgggat tctttcccga tcaccagttg gacggcggcc gcgcgcaaca cgatgaagcc 120

gtagacaaca aattcaaca agaacaaca aacgcgttct atgagatctt acatttacct 180

aacttaaacg aagaacaacg aaacgccttc atccaaagtt taaaagatga cccaagccaa 240

sequence listing_ST25.txt

```

agcgctaacc ttttagcaga agctaaaaag ctaaagatg ctcaggcgcc gaaagtagac 300
aacaattca acaaagaaca acaaacgcg ttctatgaga ttttacattt acctaactta 360
aacgaagaac aacgaaacgc cttcatccaa agtttaaaag atgacccaag ccaaagcgct 420
aaccttttag cagaagctaa aaagctaaat gatgctcagg cgccgaaagc ggccgcccct 480
gcaccgaaca tggagaacac aacatcagga ttcctaggac ccctgctcgt gttacaggcg 540
gggtttttct tgttgacaag aatcctcaca ataccacaga gtctagactc gtggtggact 600
tctctcaatt ttctaggggg agcaccacg tgtcctggcc aaaattcgca gtccccaacc 660
tccaatcact caccaacctc ttgtcctcca atttgtcctg gctatcgctg gatgtgtctg 720
cggcgtttta tcatattcct cttcatcctg ctgctatgcc tcatcttctt gttggttctt 780
ctggactacc aaggatggt gcccgtttgt cctctacttc caggaacatc aaccaccagc 840
acggggccat gcaagacctg cacgattcct gctcgaggaa cctctatggt tccctcttgt 900
tgctgtacaa aaccttcgga cagaaactgc acttgatttc ccatcccatc atcctgggct 960
ttcgcaagat tcctatggga gtgggcctca gtccgtttct cctggctcag ttactagtg 1020
ccatttggtc agtggttcgt agggctttcc cccactgttt ggctttcagt tatatggatg 1080
atgtggtatt gggggccaag tctgtacaac atcttgagtc cttttttacc tctattacca 1140
attttctttt gtctttgggt atacatt 1167

```

<210> 110

<211> 389

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (Q129R/G145R) + ZZ-tag (serotype d) sequence

<400> 110

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1           5           10           15

```

```

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20           25           30

```

```

Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu
          35           40           45

```

```

Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu
          50           55           60

```

```

Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln
65           70           75           80

```

sequence listing_ST25.txt

Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala
85 90 95

Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr
100 105 110

Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe
115 120 125

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala
130 135 140

Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro
145 150 155 160

Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu
165 170 175

Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro
180 185 190

Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala
195 200 205

Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser
210 215 220

Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu
225 230 235 240

Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe
245 250 255

Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
260 265 270

Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr
275 280 285

Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys
290 295 300

Pro Ser Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala
305 310 315 320

Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu
325 330 335

sequence listing_ST25.txt

Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr
340 345 350

Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu
355 360 365

Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys
370 375 380

Leu Trp Val Tyr Ile
385

<210> 111
<211> 966
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + EGF (serotype d) sequence

<400> 111
atgggaggtt ggtcttccaa acctcgaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa 120
tgcccgtgt ctcatgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct 180
ctggacaaat acgcatgcaa ctgtgttgta gggtacatcg gcgaacgttg ccagtatcgc 240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca 300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg gggttttctt gttgacaaga 360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcaccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct 480
tgtcctccaa ttgtcctg ctatcgtg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcaagggaac ctctatgttt ccctcttggt gctgtacaaa accttcggac 720
ggaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttggtca gtgggttcgta 840
gggctttccc ccactgtttg gctttcagtt atatggatga tgtggtattg ggggccaaagt 900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
tacatt 966

<210> 112

sequence listing_ST25.txt

<211> 322

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 + EGF (serotype d) sequence

<400> 112

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
35 40 45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
50 55 60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

sequence listing_ST25.txt

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

Tyr Ile

<210> 113
<211> 966
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R) + EGF (serotype d) sequence

<400> 113
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa 120
tgcccgtgt ctcattgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct 180
ctggacaaat acgcatgcaa ctgtgttgta ggttacatcg gcgaacgttg ccagtatcgc 240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca 300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg ggtttttctt gttgacaaga 360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcaccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct 480
tgtcctccaa ttgtcctggt ctatcgctgg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcgaggaac ctctatgttt ccctcttggt gctgtacaaa accttcggac 720

sequence listing_ST25.txt

ggaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
 tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttggtca gtggttcgta 840
 gggctttccc ccactgtttg gctttcagtt atatggatga tgtgggtattg ggggccaagt 900
 ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
 tacatt 966

<210> 114
 <211> 322
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (Q129R) + EGF (serotype d)
 sequence

<400> 114

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
 35 40 45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
 50 55 60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
 65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
 85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
 100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
 115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
 130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
 145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
 Page 100

sequence listing_ST25.txt

```

165                               170                               175
Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180                               185                               190
Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195                               200                               205
Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210                               215                               220
Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225                               230                               235
Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
240                               245                               250                               255
Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260                               265                               270
Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275                               280                               285
Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290                               295                               300
Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305                               310                               315                               320

```

Tyr Ile

<210> 115
 <211> 966
 <212> DNA
 <213> artificial sequence

<220>
 <223> 32-164 (G145R) + EGF (serotype d) sequence

```

<400> 115
atgggaggtt ggtcttccaa acctcgga aa ggc atgggga cgaatctttc tgttcccaat      60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa      120
tgcccgtgt ctc atgacgg ttactgcctg catgatggcg tatgcatgta catcgaagct      180
ctggacaaat acgcatgcaa ctgtgttgta ggttacatcg gcgaacgttg ccagtatcgc      240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca      300
acatcaggat tcctaggacc cctgctcgtg ttacaggcgg ggtttttctt gttgacaaga      360

```

sequence listing_ST25.txt

```

atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga 420
gcacccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct 480
tgtcctccaa tttgtcctgg ctatcgctgg atgtgtctgc ggcgttttat catattcctc 540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg 600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc 660
acgattcctg ctcaaggaac ctctatgttt cctctttggt gctgtacaaa accttcggac 720
agaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag 780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttgttca gtggttcgta 840
gggctttccc ccactgtttg gctttcagtt atatggatga tgtggtattg ggggccaagt 900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta 960
tacatt 966

```

<210> 116
 <211> 322
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (G145R) + EGF (serotype d) sequence

<400> 116

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20          25          30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
          35          40          45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
50          55          60

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
65          70          75          80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
          85          90          95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
100          105          110

```

sequence listing_ST25.txt

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

Tyr Ile

<210> 117

<211> 966

<212> DNA

<213> artificial sequence

<220>

<223> 32-164 (Q129R/G145R) + EGF (serotype d) sequence

sequence listing_ST25.txt

```

<400> 117
atgggagggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gacggcggcc gcatgaactc tgattccgaa    120
tgcccgtgt ctcattgacg ttactgcctg catgatggcg tatgcatgta catcgaagct    180
ctggacaaat acgcatgcaa ctgtgttgta gggtacatcg gcgaacgttg ccagtatcgc    240
gacctgaaat ggtgggaact gcgtaaggcg gccgcccctg caccgaacat ggagaacaca    300
acatcaggat tcctaggacc cctgctcgtg ttacaggcg gggttttctt gttgacaaga    360
atcctcacia taccacagag tctagactcg tgggtggactt ctctcaattt tctaggggga    420
gcacccacgt gtcctggcca aaattcgcag tccccaacct ccaatcactc accaacctct    480
tgtcctccaa tttgtcctgg ctatcgtcg atgtgtctgc ggcgttttat catattctc    540
ttcatcctgc tgctatgcct catcttcttg ttggttcttc tggactacca aggtatgttg    600
cccgtttgtc ctctacttcc aggaacatca accaccagca cggggccatg caagacctgc    660
acgattcctg ctcgaggaa ctctatgttt cctcttctgt gctgtacaaa accttcggac    720
agaaactgca cttgtattcc catcccatca tcctgggctt tcgcaagatt cctatgggag    780
tgggcctcag tccgtttctc ctggctcagt ttactagtgc catttgttca gtggttcgta    840
gggctttccc ccactgtttg gctttcagtt atatggatga tgtggtattg ggggccaagt    900
ctgtacaaca tcttgagtcc ctttttacct ctattaccaa ttttcttttg tctttgggta    960
tacatt                                           966

```

```

<210> 118
<211> 322
<212> PRT
<213> artificial sequence

```

```

<220>
<223> Proteins corresponding to 32-164 (Q129R/G145R) + EGF (serotype d)
sequence

```

<400> 118

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20          25          30

Gly Arg Met Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr
          35          40          45

Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
          50          55          60

```

sequence listing_ST25.txt

Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
65 70 75 80

Asp Leu Lys Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn
85 90 95

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
100 105 110

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
115 120 125

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
130 135 140

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
145 150 155 160

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
165 170 175

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
180 185 190

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
195 200 205

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
210 215 220

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
225 230 235 240

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
245 250 255

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
260 265 270

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
275 280 285

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
290 295 300

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
305 310 315 320

sequence listing_ST25.txt

Tyr Ile

<210> 119
<211> 825
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 + STR-tag (streptavidin) (serotype d) sequence

<400> 119
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc 120
gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc 180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt 240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa 300
aattcgcagt ccccaacctc caatcactca ccaacctctt gtcctccaat ttgtcctggc 360
tatcgctgga tgtgtctgcg gcgttttatc atattcctct tcatcctgct gctatgcctc 420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca 480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcaaggaacc 540
tctatgtttc cctcttggtg ctgtacaaaa ccttcggacg gaaactgcac ttgtattccc 600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc 660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg 720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc 780
ttttacctc tattaccaat tttcttttgt ctttgggtat acatt 825

<210> 120
<211> 275
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 32-164 + STR-tag (streptavidin)
(serotype d) sequence

<400> 120

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

sequence listing_ST25.txt

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
50 55 60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

sequence listing_ST25.txt

<210> 121
 <211> 825
 <212> DNA
 <213> artificial sequence

<220>
 <223> 32-164 (Q129R) + STR (serotype d) sequence

<400> 121
 atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc 120
 gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc 180
 ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt 240
 ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacagtg tcctggccaa 300
 aattcgcagt ccccaacctc caatcactca ccaacctctt gtcctccaat ttgtcctggc 360
 tatcgctgga tgtgtctgcg gcgttttatc atattcctct tcattcctgct gctatgcctc 420
 atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca 480
 ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcgaggaacc 540
 tctatgtttc cctcttggtg ctgtacaaaa ccttcggacg gaaactgcac ttgtattccc 600
 atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc 660
 tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg 720
 ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc 780
 tttttacctc tattaccaat tttcttttgt ctttgggtat acatt 825

<210> 122
 <211> 275
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 32-164 (Q129R) + STR (serotype d) sequence

<400> 122

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
 20 25 30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
 35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
 Page 108

sequence listing_ST25.txt

50

55

60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 123

<211> 825

<212> DNA

<213> artificial sequence

sequence listing_ST25.txt

<220>

<223> 32-164 (G145R) + STR (serotype d) sequence

<400> 123

```

atgggaggtt ggtcttccaa acctcgaaa ggcattggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc    120
gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc    180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt    240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa    300
aattcgagcgt cccaacctc caatcactca ccaacctctt gtctctcaat ttgtcctggc    360
tatcgctgga tgtgtctgcg gcgttttatt atattcctct tcattcctgt gctatgcctc    420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca    480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcaaggaacc    540
tctatgtttc cctcttggtg ctgtacaaaa ctttcggaca gaaactgcac ttgtattccc    600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc    660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg    720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc    780
tttttacctc tattaccaat tttcttttgt ctttgggtat acatt                    825

```

<210> 124

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (G145R) + STR (serotype d) sequence

<400> 124

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
          20          25          30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
          35          40          45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
          50          55          60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65          70          75          80

```

sequence listing_ST25.txt

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 125
<211> 825
<212> DNA
<213> artificial sequence

<220>
<223> 32-164 (Q129R/G145R)/STR-tag (serotype d) sequence

<400> 125

sequence listing_ST25.txt

```

atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gacggcggcc gctggagcca cccgcagttc    120
gaaaaagcgg ccgcccctgc accgaacatg gagaacacaa catcaggatt cctaggaccc    180
ctgctcgtgt tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt    240
ctagactcgt ggtggacttc tctcaatttt ctagggggag caccacgtg tcctggccaa    300
aattcgcagt ccccaacctc caatcactca ccaacctctt gtcctccaat ttgtcctggc    360
tatcgctgga tgtgtctgcg gcgttttctc atattcctct tcattcctgt gctatgcctc    420
atcttcttgt tggttcttct ggactaccaa ggtatgttgc ccgtttgtcc tctacttcca    480
ggaacatcaa ccaccagcac ggggccatgc aagacctgca cgattcctgc tcgaggaacc    540
tctatgtttc cctcttggtg ctgtacaaaa ccttcggaca gaaactgcac ttgtattccc    600
atcccatcat cctgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc    660
tggctcagtt tactagtgcc atttgttcag tggttcgtag ggctttcccc cactgtttgg    720
ctttcagtta tatggatgat gtggtattgg gggccaagtc tgtacaacat cttgagtccc    780
tttttacctc tattaccaat tttcttttgt ctttgggtat acatt                    825

```

<210> 126

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 32-164 (Q129R/G145R)/STR-tag (serotype d) sequence

<400> 126

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Gly
20 25 30

Gly Arg Trp Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro
35 40 45

Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
50 55 60

Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser
65 70 75 80

Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr
85 90 95

sequence listing_ST25.txt

Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr
100 105 110

Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg
115 120 125

Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu
130 135 140

Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro
145 150 155 160

Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro
165 170 175

Ala Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser
180 185 190

Asp Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala
195 200 205

Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu
210 215 220

Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp
225 230 235 240

Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn
245 250 255

Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp
260 265 270

Val Tyr Ile
275

<210> 127
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + ZZ (serotype d) sequence

<400> 127
atgggaggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60

cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120

ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
Page 113

sequence listing_ST25.txt

```

caacaaaacg cgttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac   240
gccttcatcc aaagttttaa agatgaccca agccaaagcg ctaacctttt agcagaagct   300
aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa   360
aacgcgttct atgagatctt acattttacct aacttaaacy aagaacaacy aaacgccttc   420
atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag   480
ctaaatgatg ctgaggcgcc gaaagcggcc gcccctgcac cgaacatgga gaacacaaca   540
tcaggattcc taggaccctt gctcgtgtta caggcggggt ttttcttggt gacaagaatc   600
ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca   660
cccacgtgtc ctggccaaaa ttgcagtcct ccaacctcca atcactcacc aacctcttgt   720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc   780
atcctgctgc tatgcctcat cttcttggtg gttcttcttg actaccaagg tatgttgccc   840
gtttgtcctc tacttccagg aacatcaacc accagcacgg ggccatgcaa gacctgcacg   900
attcctgctc aaggaacctc tatgtttccc tcttggtgct gtacaaaacc ttcggacgga   960
aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtg   1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg   1080
ctttcccca ctgtttggct ttcagttata tggatgatgt ggtattgggg gccaaagtctg   1140
tacaacatct tgagtcctt tttacctcta ttaccaattt tctttgtct ttgggtatac   1200
att                                                                    1203

```

<210> 128
 <211> 401
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 + ZZ (serotype d) sequence

<400> 128

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
 35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 50 55 60

sequence listing_ST25.txt

```

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
65              70              75              80

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85              90              95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100             105             110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115             120             125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130             135             140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145             150             155             160

Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165             170             175

Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180             185             190

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195             200             205

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210             215             220

Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225             230             235             240

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245             250             255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260             265             270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275             280             285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln
290             295             300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly
305             310             315             320

```

sequence listing_ST25.txt

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
325 330 335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 129
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R) + ZZ (serotype d) sequence

<400> 129
atgggagggtt ggtcttccaa acctcggaaa ggcatgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
caacaaaacg cggttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac 240
gccttcatcc aaagttttaa agatgaccca agccaaagcg ctaacctttt agcagaagct 300
aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa 360
aacgcgttct atgagatctt acatttacct aacttaaacg aagaacaacg aaacgccttc 420
atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag 480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca 540
tcaggattcc taggaccctt gctcgtgtta caggcggggt ttttcttggt gacaagaatc 600
ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca 660
cccacgtgtc ctggccaaaa ttgcagtc ccaacctcca atcactcacc aacctcttgt 720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc 780
atcctgctgc tatgcctcat cttcttggtg gttcttctgg actaccaagg tatgttgccc 840

sequence listing_ST25.txt

```

gtttgtcctc tacttccagg aacatcaacc accagcacgg ggccatgcaa gacctgcacg    900
attcctgctc gaggaacctc tatgtttccc tcttggtgct gtacaaaacc ttcggacgga    960
aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtgg   1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg   1080
ctttcccca ctgtttggct ttcagttata tggatgatgt ggtattgggg gccaaagtctg   1140
tacaacatct tgagtccttt tttacctcta ttaccaatth tcttttgtct ttgggtatac   1200
att                                                                    1203

```

<210> 130
 <211> 401
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R) + ZZ (serotype d)
 sequence

<400> 130

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
 35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 50 55 60

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 65 70 75 80

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
 85 90 95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
 100 105 110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
 115 120 125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
 130 135 140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
 Page 117

sequence listing_ST25.txt

```

145                      150                      155                      160
Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165                      170                      175
Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180                      185                      190
Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195                      200                      205
Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210                      215                      220
Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225                      230                      235                      240
Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245                      250                      255
Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260                      265                      270
Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275                      280                      285
Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg
290                      295                      300
Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly
305                      310                      315                      320
Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
325                      330                      335
Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340                      345                      350
Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355                      360                      365
Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370                      375                      380
Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385                      390                      395                      400

```

sequence listing_ST25.txt

file

<210> 131
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (G145R) + ZZ (serotype d) sequence

<400> 131
atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
caacaaaacg cgttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac 240
gccttcatcc aaagttaaaa agatgaccca agccaaagcg ctaacctttt agcagaagct 300
aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa 360
aacgcgttct atgagatctt acatttacct aacttaaacg aagaacaacg aaacgccttc 420
atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag 480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca 540
tcaggattcc taggaccctt gctcgtgtta caggcggggt ttttcttggt gacaagaatc 600
ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca 660
cccacgtgtc ctggccaaaa ttcgcagtcc ccaacctcca atcactcacc aacctcttgt 720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc 780
atcctgctgc tatgcctcat cttcttggtg gttcttcttg actaccaagg tatgttgccc 840
gtttgtcctc tacttccagg aacatcaacc accagcacgg ggccatgcaa gacctgcacg 900
attcctgctc aaggaacctc tatgtttccc tcttggtgct gtacaaaacc ttcggacaga 960
aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtgg 1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg 1080
ctttcccca ctgtttggtt ttcaattata tggatgatgt ggtattgggg gccaaagtctg 1140
tacaacatct tgagtccctt ttacactcta ttaccaattt tcttttgtct ttgggtatac 1200
att 1203

<210> 132
<211> 401
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 (G145R) + ZZ (serotype d)

sequence listing_ST25.txt

sequence

<400> 132

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10      15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20      25      30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
35      40      45
His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
50      55      60
Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
65      70      75      80
Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85      90      95
Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100     105     110
Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115     120     125
Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130     135     140
Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145     150     155     160
Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165     170     175
Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180     185     190
Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195     200     205
Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210     215     220
Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225     230     235     240

```

sequence listing_ST25.txt

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245 250 255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260 265 270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275 280 285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln
290 295 300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg
305 310 315 320

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
325 330 335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 133
<211> 1203
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R/G145R) + ZZ (serotype d) sequence

<400> 133
atgggaggtt ggtcttccaa acctcgaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
ccagattggg gcggccgcgc gcaacacgat gaagccgtag acaacaaatt caacaaagaa 180
caacaaaacg cgttctatga gatcttacat ttacctaact taaacgaaga acaacgaaac 240
gccttcatcc aaagtttaaa agatgaccca agccaaagcg ctaacctttt agcagaagct 300

sequence listing_ST25.txt

```

aaaaagctaa atgatgctca ggcgccgaaa gtagacaaca aattcaacaa agaacaacaa   360
aacgcgttct atgagatctt acatttacct aacttaaacg aagaacaacg aaacgccttc   420
atccaaagtt taaaagatga cccaagccaa agcgctaacc ttttagcaga agctaaaaag   480
ctaaatgatg ctcaggcgcc gaaagcggcc gccctgcac cgaacatgga gaacacaaca   540
tcaggattcc taggaccctt gctcgtgtta caggcggggt ttttcttggt gacaagaatc   600
ctcacaatac cacagagtct agactcgtgg tggacttctc tcaattttct agggggagca   660
cccacgtgtc ctggccaaaa ttcgcagtcc ccaacctcca atcactcacc aacctcttgt   720
cctccaattt gtcctggcta tcgctggatg tgtctgcggc gttttatcat attcctcttc   780
atcctgctgc tatgcctcat cttcttggtg gttcttctgg actaccaagg tatgttgccc   840
gtttgtcctc tacttccagg aacatcaacc accagcacgg ggccatgcaa gacctgcacg   900
attcctgtct gaggaacctc tatgtttccc tcttggtgct gtacaaaacc ttcggacaga   960
aactgcactt gtattcccat cccatcatcc tgggctttcg caagattcct atgggagtg   1020
gcctcagtcc gtttctcctg gctcagttta ctagtgccat ttgttcagtg gttcgtaggg   1080
ctttcccca ctgtttggct ttcagttata tggatgatgt ggtattgggg gccaaagtctg   1140
tacaacatct tgagtccctt tttacctcta ttaccaattt tcttttgtct ttgggtatac   1200
att                                                                    1203

```

<210> 134
 <211> 401
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R/G145R) + ZZ (serotype d)
 sequence

<400> 134

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Ala Gln
 35 40 45

His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
 50 55 60

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn
 65 70 75 80

sequence listing_ST25.txt

Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu
85 90 95

Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp
100 105 110

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
115 120 125

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu
130 135 140

Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys
145 150 155 160

Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn Met
165 170 175

Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala
180 185 190

Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
195 200 205

Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro
210 215 220

Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys
225 230 235 240

Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile
245 250 255

Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu
260 265 270

Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr
275 280 285

Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg
290 295 300

Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg
305 310 315 320

Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe
Page 123

sequence_listing_ST25.txt

325

330

335

Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val
340 345 350

Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser
355 360 365

Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu
370 375 380

Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
385 390 395 400

Ile

<210> 135
<211> 1002
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + EGF (serotype d) sequence

<400> 135
atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgcat gaactctgat tccgaatgcc cgctgtctca tgacggttac 180
tgcctgcatg atggcgtatg catgtacatc gaagctcttg acaatacgc atgcaactgt 240
gttgtaggtt acatcggcga acgttgccag tatcgcgacc tgaaatggtg ggaactgcgt 300
aaggcggccg cccctgcacc gaacatggag aacacaacat caggattcct aggaccctg 360
ctcgtgttac aggcggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta 420
gactcgtggt ggacttctct caattttcta gggggagcac ccacgtgtcc tggccaaaat 480
tcgcagtccc caacctcaa tcactacca acctcttgtc ctccaatttg tcctggctat 540
cgctggatgt gtctgcggcg ttttatcata ttctcttca tcctgctgct atgcctcatc 600
ttcttggttg ttcttctgga ctaccaaggt atgttgcccg tttgtcctct acttccagga 660
acatcaacca ccagcacggg gccatgcaag acctgcacga ttctgctca aggaacctct 720
atgtttccct cttgttgctg taaaaacct tcggacggaa actgcacttg tattcccatc 780
ccatcatcct gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg 840
ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggctt 900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcccttt 960

sequence listing_ST25.txt

ttacctctat taccaatttt cttttgtctt tgggtataca tt

1002

<210> 136

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 + EGF (serotype d) sequence

<400> 136

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
35 40 45

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
50 55 60

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
65 70 75 80

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
85 90 95

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
130 135 140

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
Page 125

195

<210>	137
<211>	1002
<212>	DNA
<213>	artificial sequence

<220>
<223> 44-164 (Q129R) + EGF (serotype d) sequence

<400>	137						
atgggaggtt	ggtcttccaa	acctcgga	aaa ggc	atgggga	cgaatctttc	tgttcccaat	60
cctctgggat	tctttcccga	tcaccagttg	gaccctgcgt	tcggagccaa	ctcaaacaat		120
ccagattggg	gcggccgcat	gaactctgat	tccgaatgcc	cgctgtctca	tgacggttac		180
tgcttgcagt	atggcgatat	catgtacatc	gaagctcttg	acaatacgc	atgcaactgt		240
gtttaggtt	acatcggcga	acgttgccag	tatcgcgacc	tgaaatggtg	ggaactgcgt		300
aaggcggccg	cccctgcacc	gaacatggag	aacacaacat	caggattcct	aggacctctg		360
ctcgtgttac	aggcgggggt	tttcttgttg	acaagaatcc	tcacaatacc	acagagtcta		420
gactcgtggt	ggacttctct	caattttcta	gggggagcac	ccacgtgtcc	tggccaaaat		480
tcgcagtccc	caacctccaa	tcactcacca	acctcttgtc	ctccaatttg	tcctggctat		540
cgctggatgt	gtctgcggcg	tttatcata	ttctctttca	tcctgctgct	atgcctcatc		600

sequence listing_ST25.txt

```

ttcttggttg ttcttctgga ctaccaaggt atgttgcccg tttgtcctct acttccagga    660
acatcaacca ccagcacggg gccatgcaag acctgcacga ttctgctcg aggaacctct    720
atgtttccct cttgttgctg tacaaaacct tcggacggaa actgcacttg tattcccatc    780
ccatcatcct gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg    840
ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggtt    900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcccttt    960
ttacctctat taccaatctt cttttgtctt tgggtataca tt                    1002

```

<210> 138
 <211> 334
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R) + EGF (serotype d)
 sequence

<400> 138

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
 35 40 45

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 50 55 60

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 65 70 75 80

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 85 90 95

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
 100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
 115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
 130 135 140

sequence listing_ST25.txt

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
290 295 300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 139
<211> 1002
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (G145R) + EGF (serotype d) sequence

<400> 139
atgggaggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
ccagattggg gcggccgcga gaactctgat tccgaatgcc cgctgtctca tgacggttac 180

sequence listing_ST25.txt

```

tgctgcatg atggcgatg catgtacatc gaagctctgg acaatacgc atgcaactgt 240
gtttaggtt acatcggcga acgttgccag tatcgcgacc tgaaatggtg ggaactgcgt 300
aaggcggccg cccctgcacc gaacatggag aacacaacat caggattcct aggacccctg 360
ctcgtgttac aggcggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta 420
gactcgtggt ggactttctt caattttcta gggggagcac ccacgtgtcc tggccaaaat 480
tcgcagtccc caacctcaa tcactcacca acctcttgct ctccaatttg tcctggctat 540
cgctggatgt gtctgcggcg ttttatcata ttctcttca tcctgctgct atgcctcatc 600
ttcttggttg ttcttctgga ctaccaaggt atgttgcccg ttgtcctct acttccagga 660
acatcaacca ccagcacggg gccatgcaag acctgcacga ttctgctca aggaacctct 720
atgtttccct cttgttgctg taaaaacct tcggacagaa actgcacttg tattcccatc 780
ccatcatcct gggctttcgc aagattccta tgggagtggg cctcagtccg tttctcctgg 840
ctcagtttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac tgtttggtt 900
tcagttatat ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcccttt 960
ttacctctat taccaatttt cttttgtctt tgggtataca tt 1002

```

<210> 140

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 (G145R) + EGF (serotype d)
sequence

<400> 140

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1           5           10          15

```

```

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30

```

```

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
          35          40          45

```

```

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
          50          55          60

```

```

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
65          70          75          80

```

```

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
          85          90          95

```

sequence listing_ST25.txt

Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
100 105 110

Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
115 120 125

Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
130 135 140

Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
145 150 155 160

Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
165 170 175

Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
180 185 190

Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
195 200 205

Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
210 215 220

Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser
225 230 235 240

Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr
245 250 255

Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
260 265 270

Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
275 280 285

Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp
290 295 300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 141
<211> 1002

sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 44-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 141

```

atgggagggtt ggtcttccaa acctcgga aa ggcattggga cgaatctttc tgttcccaat      60
cctctgggat  tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat      120
ccagattggg  gcggccgcat gaactctgat tccgaatgcc cgctgtctca tgacggttac      180
tgcctgcatg  atggcgtatg catgtacatc gaagctctgg acaaatacgc atgcaactgt      240
gttgtaggtt  acatcggcga acgttgccag tatcgcgacc tgaaatggtg ggaactgcgt      300
aaggcggccg  cccctgcacc gaacatggag aacacaacat caggattcct aggacccttg      360
ctcgtgttac  aggcgggggtt tttcttggtg acaagaatcc tcacaatacc acagagtcta      420
gactcgtggt  ggacttctct caattttcta gggggagcac ccacgtgtcc tggccaaaat      480
tcgcagtccc  caacctccaa tcactcacca acctcttgtc ctccaatttg tcctggctat      540
cgctggatgt  gtctgcggcg ttttatcata ttctcttca tcctgctgct atgcctcatc      600
ttcttggttg  ttcttctgga ctaccaaggt atgttgcccg tttgtcctct acttccagga      660
acatcaacca  ccagcacggg gccatgcaag acctgcacga ttctgctcg aggaacctct      720
atgtttccct  cttgttgctg taaaaaacct tcggacagaa actgcacttg tattcccatc      780
ccatcatcct  gggctttcgc aagattccta tgggagtggg cctcagtcgg tttctcctgg      840
ctcagtttac  tagtgccatt tgttcagtg ttcgtagggc tttccccac tgtttggctt      900
tcagttatat  ggatgatgtg gtattggggg ccaagtctgt acaacatctt gagtcctttt      960
ttacctctat  taccaatttt cttttgtctt tgggtatata tt                                1002

```

<210> 142

<211> 334

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 44-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 142

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1          5          10          15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Met Asn
 35          40          45

```

sequence_listing_ST25.txt

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
 50 55 60
 Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys
 65 70 75 80
 Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp
 85 90 95
 Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr
 100 105 110
 Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe
 115 120 125
 Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp
 130 135 140
 Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn
 145 150 155 160
 Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile
 165 170 175
 Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu
 180 185 190
 Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr
 195 200 205
 Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr
 210 215 220
 Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser
 225 230 235 240
 Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys Thr
 245 250 255
 Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu
 260 265 270
 Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val
 275 280 285
 Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp

sequence listing_ST25.txt

290

295

300

Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe
305 310 315 320

Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
325 330

<210> 143
<211> 861
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 + STR-tag (serotype d) sequence

<400> 143
atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg 180
aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcggggttt 240
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
cactcacaa cctcttgctc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggtggt tcttctggac 480
taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 540
ccatgcaaga cctgcacgat tcctgctcaa ggaacctcta tgtttcctc ttgttgctgt 600
acaaaacctt cggacggaaa ctgcatttgt attcccatcc catcatcctg ggctttcgca 660
agattcctat gggagtgggc ctcagtcctg ttctcctggc tcagtttact agtgccattt 720
gttcagtgtg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 780
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 840
ttttgtcttt gggatacat t 861

<210> 144
<211> 287
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 + STR-tag (serotype d) sequence

<400> 144

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro

260

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
275 280 285

<210> 145
<211> 861
<212> DNA
<213> artificial sequence

<220>
<223> 44-164 (Q129R) + STR-tag (serotype d) sequence

<400> 145
atgggagggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tggtcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg gcggccgctg gagccaccg cagttcgaaa aagcggccgc ccctgcaccg 180
aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 240
ttcttgttga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac 480
taccaaggta tggtgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacggg 540
ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttggtgctgt 600
acaaaacctt cggacggaaa ctgcattgt attcccatcc catcatcctg ggctttcgca 660
agattcctat gggagtgggc ctgagtcctt ttctcctggc tcagtttact agtgccattt 720
gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 780
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 840
ttttgtcttt gggtatacat t 861

<210> 146
<211> 287
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 44-164 (Q129R) + STR-tag (serotype d) sequence

<400> 146

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
Page 135

sequence listing_ST25.txt

20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
260 265 270

sequence listing_ST25.txt

Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile
	275						280					285		

<210> 147
 <211> 861
 <212> DNA
 <213> artificial sequence

<220>
 <223> 44-164 (G145R) + STR-tag (serotype d) sequence

<400> 147

atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat	60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat	120
ccagattggg gcggccgctg gagccacccg cagttcgaaa aagcggccgc ccctgcaccg	180
aacatggaga acacaacatc aggattccta ggaccctcgc tcgtgttaca ggcgggggtt	240
ttcttggtga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc	300
aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat	360
cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt	420
tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttgttggt tcttctggac	480
taccaaggta tgttgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg	540
ccatgcaaga cctgcacgat tcctgctcaa ggaacctcta tgtttccctc ttgttgctgt	600
acaaaacctt cggacagaaa ctgcacttgt attcccatcc catcatcctg ggctttcgca	660
agattcctat gggagtgggc ctgagtcgt ttctcctggc tcagtttact agtgccattt	720
gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg	780
tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc	840
ttttgtcttt gggatacat t	861

<210> 148
 <211> 286
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (G145R) + STR-tag (serotype d) sequence

<400> 148

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu
1				5					10					15	

Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro
			20					25					30		

sequence listing_ST25.txt

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
35 40 45

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
50 55 60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65 70 75 80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
85 90 95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
100 105 110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
115 120 125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
130 135 140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145 150 155 160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
165 170 175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
180 185 190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
195 200 205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
210 215 220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225 230 235 240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
245 250 255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
260 265 270

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr
275 280 285

sequence listing_ST25.txt

<210> 149
 <211> 861
 <212> DNA
 <213> artificial sequence

<220>
 <223> 44-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 149
 atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg gcggccgctg gagccacccg cagttcga aaagcggccgc ccctgcaccg 180
 aacatggaga acacaacatc aggattccta ggacccctgc tcgtgttaca ggcgggggtt 240
 ttcttgttga caagaatcct cacaatacca cagagtctag actcgtggtg gacttctctc 300
 aattttctag ggggagcacc cacgtgtcct ggccaaaatt cgcagtcccc aacctccaat 360
 cactcaccaa cctcttgtcc tccaatttgt cctggctatc gctggatgtg tctgcggcgt 420
 tttatcatat tcctcttcat cctgctgcta tgcctcatct tcttggttgg tcttctggac 480
 taccaaggta tgttgcccgt ttgtcctcta cttccaggaa catcaaccac cagcacgggg 540
 ccatgcaaga cctgcacgat tcctgctcga ggaacctcta tgtttccctc ttggttgcgt 600
 acaaaacctt cggacagaaa ctgcattgt attcccatcc catcatcctg ggctttcgca 660
 agattcctat gggagtgggc ctgagtcctg ttctcctggc tcagtttact agtgccattt 720
 gttcagtggg tcgtagggct ttccccact gtttggtttt cagttatatg gatgatgtgg 780
 tattgggggc caagtctgta caacatcttg agtccctttt tacctctatt accaattttc 840
 ttttgtcttt gggatacat t 861

<210> 150
 <211> 287
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 44-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 150

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Gly Gly Arg Trp Ser
 35 40 45

sequence listing_ST25.txt

```

His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
 50          55          60

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
65          70          75          80

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
      85          90          95

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
      100          105          110

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
      115          120          125

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
      130          135          140

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
145          150          155          160

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
      165          170          175

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
      180          185          190

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
      195          200          205

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
      210          215          220

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
225          230          235          240

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
      245          250          255

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
      260          265          270

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
      275          280          285

<210> 151
<211> 1254

```


sequence listing_ST25.txt

<212> DNA

<213> artificial sequence

<220>

<223> 61-164 + ZZ (serotype d) sequence

<400> 151

```

atgggagggtt ggtcttccaa acctcgga aa ggcattggga cgaatctttc tgttcccaat    60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat    120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg    180
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac    240
gcgttctatg agatcttaca tttacctaac ttaaacgaag aacaacgaaa cgccttcatc    300
caaagttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta    360
aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc    420
tatgagatct tacatttacc taacttaa ac gaagaacaac gaaacgcctt catccaaagt    480
ttaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat    540
gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc    600
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata    660
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt    720
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt    780
tgtcctggct atcgctggat gtgtctgcgg cgttttatca tattcctctt catcctgctg    840
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct    900
ctacttcag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct    960
caaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact   1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc   1080
cgtttctcct ggctcagttt actagtacca tttgttcagt ggttcgtagg gctttccccc   1140
actgtttggc tttcagttat atggatgatg tggatattgg ggccaagtct gtacaacatc   1200
ttgagtcctt tttacctct attaccaatt ttcttttgc tttgggtata catt         1254

```

<210> 152

<211> 418

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 + ZZ (serotype d) sequence

<400> 152

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

```

sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
85 90 95

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100 105 110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115 120 125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130 135 140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145 150 155 160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165 170 175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180 185 190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195 200 205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210 215 220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
225 230 235 240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245 250 255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260 265 270

sequence listing_ST25.txt

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
275 280 285
Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290 295 300
Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305 310 315 320
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325 330 335
Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
340 345 350
Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
355 360 365
Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
370 375 380
Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
385 390 395 400
Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
405 410 415

Tyr Ile

<210> 153
<211> 1254
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R) + ZZ (serotype d) sequence

<400> 153
atgggagggtt ggtcttccaa acctcggaag ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
ccagattggg acttcaacc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac 300
caaagtttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360

sequence listing_ST25.txt

```

aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc 420
tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
ttaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat 540
gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 720
cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt 780
tgtcctggct atcgctggat gtgtctgcgg cgttttatca ttttctctt catcctgctg 840
ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgtcct 900
ctacttccag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct 960
cgaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact 1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc 1080
cgtttctcct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttcccc 1140
actgtttggc tttcagttat atggatgatg tggattggg ggccaagtct gtacaacatc 1200
ttgagtcctt tttacctct attaccaatt ttcttttgtc tttgggtata catt 1254

```

<210> 154
 <211> 418
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (Q129R) + ZZ (serotype d) sequence

<400> 154

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
 50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
 65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
 Page 144

sequence_listing_ST25.txt

85

90

95

```

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100      105      110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115      120      125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130      135      140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145      150      155      160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165      170      175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180      185      190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195      200      205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210      215      220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
225      230      235      240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245      250      255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260      265      270

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
275      280      285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290      295      300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305      310      315      320

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325      330      335

```

sequence listing_ST25.txt

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
 340 345 350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
 355 360 365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
 370 375 380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
 385 390 395 400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
 405 410 415

Tyr Ile

<210> 155
 <211> 1254
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (G145R) + ZZ (serotype d) sequence

<400> 155
 atgggagggtt ggtcttccaa acctcggaag ggcattgggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcgggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
 gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcac 300
 caaagtttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360
 aatgatgctc aggcgcccga agtagacaac aaattcaaca agaacaaca aaacgcgttc 420
 tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
 ttaaaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat 540
 gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
 ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
 ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 720
 cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt 780
 tgcctgggt atcgtggat gtgtctgcgg cgttttatca tattcctctt catcctgctg 840
 ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct 900

sequence listing_ST25.txt

```
ctactttccag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct    960
caaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacag aaactgcact    1020
tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc    1080
cgtttctcct ggctcagttt actagtgcc a tttgttcagt ggttcgtagg gctttccccc    1140
actgtttggc tttcagttat atggatgatg tgggtattggg ggccaagtct gtacaacatc    1200
ttgagtcctt ttttacctct attaccaatt ttcttttgtc tttgggtata catt        1254
```

<210> 156
 <211> 418
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (G145R) + ZZ (serotype d) sequence

<400> 156

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
 50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
 65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
 85 90 95

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
 100 105 110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
 115 120 125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
 130 135 140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
 145 150 155 160

sequence_listing_ST25.txt

```

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
      165      170      175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
      180      185      190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
      195      200      205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
      210      215      220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
225      230      235      240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
      245      250      255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
      260      265      270

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
      275      280      285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290      295      300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305      310      315      320

Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
      325      330      335

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
      340      345      350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
355      360      365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
370      375      380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
385      390      395      400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
405      410      415

```


sequence listing_ST25.txt

Tyr Ile

<210> 157
 <211> 1254
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (Q129R/G145R) + ZZ (serotype d) sequence

<400> 157
 atgggaggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcggccgcg cgcaacacga tgaagccgta gacaacaaat tcaacaaaga acaacaaaac 240
 gcgttctatg agatcttaca ttacctaac ttaaacgaag aacaacgaaa cgccttcatt 300
 caaagtttaa aagatgacct aagccaaagc gctaaccttt tagcagaagc taaaaagcta 360
 aatgatgctc aggcgcccga agtagacaac aaattcaaca aagaacaaca aaacgcgttc 420
 tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt 480
 ttaaaagatg acccaagcca aagcgctaac ctttttagcag aagctaaaaa gctaaatgat 540
 gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc 600
 ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata 660
 ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt 720
 cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tctccaatt 780
 tgtcctggct atcgtctgat gtgtctgcgg cgttttatca ttttctctt catcctgctg 840
 ctatgcctca tcttcttggt ggttcttctg gactaccaag gtatgttgcc cgtttgcct 900
 ctacttcag gaacatcaac caccagcacg gggccatgca agacctgcac gattcctgct 960
 cgaggaacct ctatgtttcc ctcttggtgc tgtacaaaac cttcggacag aaactgcact 1020
 tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc 1080
 cgtttctcct ggctcagttt actagtgcc tttgttcagt ggttcgtagg gctttcccc 1140
 actgtttggc tttcagttat atggatgatg tggattggg ggccaagtct gtacaacatc 1200
 ttgagtcctt tttacctct attaccaatt ttctttgtc tttgggtata catt 1254

<210> 158
 <211> 418
 <212> PRT
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> Proteins corresponding to 61-164 (Q129R/G145R) + ZZ (serotype d)
sequence

<400> 158

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Ala
50 55 60

Gln His Asp Glu Ala Val Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
65 70 75 80

Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg
85 90 95

Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
100 105 110

Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val
115 120 125

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
130 135 140

His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser
145 150 155 160

Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
165 170 175

Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Ala Ala Pro Ala Pro Asn
180 185 190

Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
195 200 205

Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu
210 215 220

Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
Page 150

sequence listing_ST25.txt

225 230 235 240

Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
245 250 255

Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
260 265 270

Ile Ile Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val
275 280 285

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
290 295 300

Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
305 310 315 320

Arg Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
325 330 335

Arg Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg
340 345 350

Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu
355 360 365

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
370 375 380

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
385 390 395 400

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
405 410 415

Tyr Ile

<210> 159
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 + EGF (serotype d) sequence

<400> 159
atgggagggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60

cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaacaat 120
Page 151

sequence listing_ST25.txt

```

ccagattggg acttcaaccc caacaaggat caatggccag aggcaaata ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 360
gcccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
caggcggggg ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 720
accagcacgg ggccatgcaa gacctgcacg attcctgtctc aaggaacctc tatgtttccc 780
tcttggtgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc 840
tgggctttcg caagattcct atgggagtg gcttcagtcc gtttctcctg gctcagttta 900
ctagtgccat ttgttcagt gttcgtagg ctttcccca ctgtttggct ttcagttata 960
tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtccttt tttacctcta 1020
ttaccaattt tcttttgtct ttgggtatac att 1053

```

<210> 160

<211> 351

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 + EGF (serotype d) sequence

<400> 160

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1          5          10          15

```

```

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
          20          25          30

```

```

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
          35          40          45

```

```

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
          50          55          60

```

```

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
65          70          75          80

```

sequence listing_ST25.txt

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
85 90 95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
100 105 110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
115 120 125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
130 135 140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
145 150 155 160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
165 170 175

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
180 185 190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
195 200 205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
210 215 220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
225 230 235 240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
245 250 255

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

sequence listing_ST25.txt

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 340 345 350

<210> 161
 <211> 1053
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (Q129R) + EGF (serotype d) sequence

<400> 161
 atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 240
 gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
 tacatcggcg aacgttgcca gtatcgcgac ctgaaatggt gggaactgcg taaggcggcc 360
 gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
 caggcggggg ttttcttggt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
 tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
 ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
 tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
 gttcttcttg actaccaagg tatgttgccc gtttgtcctc tacttccagg aacatcaacc 720
 accagcacgg ggccatgcaa gacctgcacg attcctgctc gaggaacctc tatgtttccc 780
 tcttggtgct gtacaaaacc ttcggacgga aactgcactt gtattcccat cccatcatcc 840
 tgggctttcg caagattcct atgggagtg gacctcagtc gtttctcctg gctcagttta 900
 ctagtgccat ttgttcagtg gttcgtaggg ctttccccca ctgtttggct ttcagttata 960
 tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtccttt ttacctcta 1020
 ttaccaattt tcttttgtct ttgggtatac att 1053

<210> 162
 <211> 351
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (Q129R) + EGF (serotype d) sequence

<400> 162

sequence_listing_ST25.txt

```

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1      5      10      15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
      20      25      30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
      35      40      45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
      50      55      60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
      65      70      75      80

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
      85      90      95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
      100      105      110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
      115      120      125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
      130      135      140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
      145      150      155      160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
      165      170      175

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
      180      185      190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
      195      200      205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
      210      215      220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
      225      230      235      240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
      245      250      255

```

sequence_listing_ST25.txt

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
340 345 350

<210> 163
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (G145R) + EGF (serotype d) sequence

<400> 163
atgggaggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacgggta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatacg catgcaactg tgttgtaggt 300
tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaactgcg taaggcggcc 360
gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
caggcggggg ttttcttggt gacaagaatc ctcaatac cacagagtct agactcgtgg 480
tggaattctc tcaattttct agggggagca ccacgtgtc ctggccaaaa ttcgcagtcc 540
ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttggtg 660
gttcttctgg actaccaagg tatgttgccc gtttgctctc tacttccagg aacatcaacc 720
accagcacgg ggccatgcaa gacctgcag attcctgctc aaggaacctc tatgtttccc 780
tcttgttgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 840
tgggctttcg caagattcct atgggagtg gacctagtc gtttctcctg gctcagttta 900

sequence listing_ST25.txt

ctagtgccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggct ttcagttata 960
 tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 1020
 ttaccaattt tcttttgtct ttgggtatac att 1053

<210> 164
 <211> 351
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to61-164 (G145R) + EGF (serotype d)
 sequence

<400> 164

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
 50 55 60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 65 70 75 80

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 85 90 95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
 100 105 110

Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
 115 120 125

Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
 130 135 140

Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
 145 150 155 160

Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
 165 170 175

sequence listing_ST25.txt

Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
180 185 190

Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
195 200 205

Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
210 215 220

Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
225 230 235 240

Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr
245 250 255

Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
260 265 270

Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285

Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300

Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320

Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335

Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
340 345 350

<210> 165
<211> 1053
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R/G145R) + EGF (serotype d) sequence

<400> 165
atgggagggtt ggtcttccaa acctcgga aa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaacc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgca tgaactctga ttccgaatgc ccgctgtctc atgacggtta ctgcctgcat 240
gatggcgtat gcatgtacat cgaagctctg gacaaatagc catgcaactg tgttgtaggt 300

sequence listing_ST25.txt

tacatcggcg aacgttgcca gtatcgcgac ctgaaatggg gggaaactgcg taaggcggcc 360
 gccctgcac cgaacatgga gaacacaaca tcaggattcc taggaccctt gctcgtgtta 420
 caggcgggggt ttttcttgtt gacaagaatc ctcacaatac cacagagtct agactcgtgg 480
 tggacttctc tcaattttct agggggagca cccacgtgtc ctggccaaaa ttcgcagtcc 540
 ccaacctcca atcactcacc aacctcttgt cctccaattt gtcctggcta tcgctggatg 600
 tgtctgcggc gttttatcat attcctcttc atcctgctgc tatgcctcat cttcttgttg 660
 gttcttctgg actaccaagg tatgttgccc gtttgcctc tacttccagg aacatcaacc 720
 accagcacgg ggccatgcaa gacctgcacg attcctgctc gaggaacctc tatgtttccc 780
 tcttgttgct gtacaaaacc ttcggacaga aactgcactt gtattcccat cccatcatcc 840
 tgggctttcg caagattcct atgggagtg gctcagtcg gtttctcctg gctcagttta 900
 ctagtgccat ttgttcagtg gttcgtaggg ctttcccca ctgtttggct ttcagttata 960
 tggatgatgt ggtattgggg gccaaagtctg tacaacatct tgagtcctt tttacctcta 1020
 ttaccaattt tcttttgtct ttgggtatac att 1053

<210> 166

<211> 351

<212> PRT

<213> artificial sequence

<220>

<223> Proteins corresponding to 61-164 (Q129R/G145R) + EGF (serotype d)
 sequence

<400> 166

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
 1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Met
 50 55 60

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
 65 70 75 80

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
 85 90 95

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
 Page 159

sequence listing_ST25.txt
105 110

100
Trp Trp Glu Leu Arg Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn
115 120 125
Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe
130 135 140
Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp
145 150 155 160
Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln
165 170 175
Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro
180 185 190
Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe
195 200 205
Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp
210 215 220
Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr
225 230 235 240
Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr
245 250 255
Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn Cys
260 265 270
Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp
275 280 285
Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe
290 295 300
Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile
305 310 315 320
Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro
325 330 335
Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
340 345 350

sequence listing_ST25.txt

<210> 167
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 + STR-tag (serotype d) sequence

<400> 167
atgggagggtt ggtcttccaa acctcggaaa ggcattgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggacccctg ctcgtgttac aggcgggggtt tttcttggtg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtcac caacctccaa tcactcacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttcagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttctgtctca aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
tgggagtggt cctcagtcg tttctcctgg ctcagtttac tagtgccatt tgttcagtg 780
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtatata tt 912

<210> 168
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 + STR-tag (serotype d) sequence

<400> 168

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15
Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30
Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

sequence listing_ST25.txt

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
 50 55 60
 Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
 65 70 75 80
 Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 85 90 95
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 100 105 110
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 115 120 125
 Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 130 135 140
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 145 150 155 160
 Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 165 170 175
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 180 185 190
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 195 200 205
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 210 215 220
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 225 230 235 240
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 245 250 255
 Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 260 265 270
 Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 275 280 285
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 290 295 300

sequence listing_ST25.txt

<210> 169
 <211> 912
 <212> DNA
 <213> artificial sequence

<220>
 <223> 61-164 (Q129R) + STR-tag (serotype d) sequence

<400> 169
 atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
 cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
 ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
 ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
 aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttgttg 300
 acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
 gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcaactacca 420
 acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
 ttctcttca tcctgctgct atgcctcatc ttcttgttgg ttcttctgga ctaccaaggt 540
 atgttgccc tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 600
 acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 660
 tcggacggaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
 tgggagtggg cctcagtccg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
 ttctgtagggc tttcccccac tgtttggtt tcagttatat ggatgatgtg gtattggggg 840
 ccaagtctgt acaacatctt gagtcccttt ttaccttat taccaatttt cttttgtctt 900
 tgggtataca tt 912

<210> 170
 <211> 304
 <212> PRT
 <213> artificial sequence

<220>
 <223> Proteins corresponding to 61-164 (Q129R) + STR-tag (serotype d) sequence

<400> 170

Met	Gly	Gly	Trp	Ser	Ser	Lys	Pro	Arg	Lys	Gly	Met	Gly	Thr	Asn	Leu
1				5					10					15	
Ser	Val	Pro	Asn	Pro	Leu	Gly	Phe	Phe	Pro	Asp	His	Gln	Leu	Asp	Pro
			20					25					30		

sequence_listing_ST25.txt

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
260 265 270

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

sequence listing_ST25.txt

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 171
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (G145R) + STR-tag (serotype d) sequence

<400> 171
atgggaggtt ggtcttccaa acctcggaaa ggcattggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggacccttg ctcgtgttac aggcgggggtt tttcttggtg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctccaa tctctacca 420
acctcttgct ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttcctcttca tcctgctgct atgcctcatc ttcttggttg ttcttctgga ctaccaaggt 540
atgttgcccc tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttctgctca aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacagaa actgcacttg tattcccatc ccatcatcct gggctttcgc aagattccta 720
tgggagtggt cctcagtcct tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtataca tt 912

<210> 172
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 (G145R) + STR-tag (serotype d) sequence

<400> 172

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
Page 165

sequence listing_ST25.txt

20

25

30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
260 265 270

sequence listing_ST25.txt

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 173
<211> 912
<212> DNA
<213> artificial sequence

<220>
<223> 61-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 173
atgggagggtt ggtcttccaa acctcggaaa ggcatgggga cgaatctttc tgttcccaat 60
cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat 120
ccagattggg acttcaaccc caacaaggat caatggccag aggcaaatca ggtaggagcg 180
ggcggccgct ggagccaccc gcagttcgaa aaagcggccg cccctgcacc gaacatggag 240
aacacaacat caggattcct aggaccctg ctcgtgttac aggcgggggtt tttcttgttg 300
acaagaatcc tcacaatacc acagagtcta gactcgtggt ggacttctct caattttcta 360
gggggagcac ccacgtgtcc tggccaaaat tcgcagtccc caacctcaa tcactcacca 420
acctcttgtc ctccaatttg tcctggctat cgctggatgt gtctgcggcg ttttatcata 480
ttctcttca tcctgctgct atgcctcatc ttcttgttggt ttcttctgga ctaccaaggt 540
atgttgcccg tttgtcctct acttccagga acatcaacca ccagcacggg gccatgcaag 600
acctgcacga ttctgctcg aggaacctct atgtttccct cttgttgctg tacaaaacct 660
tcggacagaa actgcacttg tattcccatc ccatactctt gggctttcgc aagattccta 720
tgggagtggt cctcagtccg tttctcctgg ctcagtttac tagtgccatt tgttcagtgg 780
ttcgtagggc tttccccac tgtttggctt tcagttatat ggatgatgtg gtattggggg 840
ccaagtctgt acaacatctt gagtcccttt ttacctctat taccaatttt cttttgtctt 900
tgggtataca tt 912

<210> 174
<211> 304
<212> PRT
<213> artificial sequence

<220>
<223> Proteins corresponding to 61-164 (Q129R/G145R) + STR-tag (serotype d) sequence

<400> 174

Met Gly Gly Trp Ser Ser Lys Pro Arg Lys Gly Met Gly Thr Asn Leu
1 5 10 15

sequence listing_ST25.txt

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp Gln Trp Pro Glu Ala Asn Gln Val Gly Ala Gly Gly Arg Trp
50 55 60

Ser His Pro Gln Phe Glu Lys Ala Ala Ala Pro Ala Pro Asn Met Glu
65 70 75 80

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
85 90 95

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
100 105 110

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
115 120 125

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
130 135 140

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
145 150 155 160

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
165 170 175

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
180 185 190

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly
195 200 205

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Arg Asn
210 215 220

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
225 230 235 240

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
245 250 255

Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val
Page 168

sequence listing_ST25.txt
265 270

260

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
275 280 285

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
290 295 300

<210> 175
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-1

<400> 175
atggcctcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc 120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg ccagataaac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggta ccttatgggc 540
agcatgaccc ccaggccgtg gctggcgttc gtggccctca tcccgccgac cttgcccggc 600
accaacatcg tgcttggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct ggacctggct atgctggctg cgattcgccg cgtttacggg 720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggactgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc ccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
tccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg 1080
atatgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

<210> 176
<211> 1128
<212> PRT
<213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-2

<400> 176

Ala Thr Gly Gly Cys Thr Thr Cys Gly Thr Ala Cys Cys Cys Cys Thr
1 5 10 15

Gly Cys Cys Ala Thr Cys Ala Ala Cys Ala Cys Gly Cys Gly Thr Cys
20 25 30

Thr Gly Cys Gly Thr Thr Cys Gly Ala Cys Cys Ala Gly Gly Cys Thr
35 40 45

Gly Cys Gly Cys Gly Thr Thr Cys Thr Cys Gly Cys Gly Gly Cys Cys
50 55 60

Ala Thr Ala Gly Cys Ala Ala Cys Cys Gly Ala Cys Gly Thr Ala Cys
65 70 75 80

Gly Gly Cys Gly Thr Thr Gly Cys Gly Cys Cys Cys Thr Cys Gly Cys
85 90 95

cys Gly Gly Cys Ala Gly Cys Ala Ala Gly Ala Ala Gly Cys Cys Ala
100 105 110

cys Gly Gly Ala Ala Gly Thr Cys Cys Gly Cys Cys Thr Gly Gly Ala
115 120 125

Gly Cys Ala Gly Ala Ala Ala Ala Thr Gly Cys Cys Cys Ala Cys Gly
130 135 140

Cys Thr Ala Cys Thr Gly Cys Gly Gly Gly Thr Thr Thr Ala Thr Ala
145 150 155 160

Thr Ala Gly Ala Cys Gly Gly Thr Cys Cys Thr Cys Ala Cys Gly Gly
165 170 175

Gly Ala Thr Gly Gly Gly Gly Ala Ala Ala Ala Cys Cys Ala Cys Cys
180 185 190

Ala Cys Cys Ala Cys Gly Cys Ala Ala Cys Thr Gly Cys Thr Gly Gly
195 200 205

Thr Gly Gly Cys Cys Cys Thr Gly Gly Gly Thr Thr Cys Gly Cys Gly
210 215 220

Cys Gly Ala Cys Gly Ala Thr Ala Thr Cys Gly Thr Cys Thr Ala Cys
Page 170

sequence listing_ST25.txt															
225				230				235				240			
Gly	Thr	Ala	Cys	Cys ₂₄₅	Cys	Gly	Ala	Gly	Cys ₂₅₀	Cys	Gly	Ala	Thr	Gly ₂₅₅	Ala
Cys	Thr	Thr	Ala ₂₆₀	Cys	Thr	Gly	Gly	Cys ₂₆₅	Ala	Gly	Gly	Thr	Gly ₂₇₀	Cys	Thr
Gly	Gly	Gly ₂₇₅	Gly	Gly	Cys	Thr	Thr ₂₈₀	Cys	Cys	Gly	Ala	Gly ₂₈₅	Ala	Cys	Ala
Ala	Thr ₂₉₀	Cys	Gly	Cys	Gly	Ala ₂₉₅	Ala	Cys	Ala	Thr	Cys ₃₀₀	Thr	Ala	Cys	Ala
Cys ₃₀₅	Cys	Ala	Cys	Ala	Cys ₃₁₀	Ala	Ala	Cys	Ala	Cys ₃₁₅	Cys	Gly	Cys	Cys	Thr ₃₂₀
Cys	Gly	Ala	Cys	Cys ₃₂₅	Ala	Gly	Gly	Gly	Thr ₃₃₀	Gly	Ala	Gly	Ala	Thr ₃₃₅	Ala
Thr	Cys	Gly	Gly ₃₄₀	Cys	Cys	Gly	Gly	Gly ₃₄₅	Gly	Ala	Cys	Gly	Cys ₃₅₀	Gly	Gly
Cys	Gly	Gly ₃₅₅	Thr	Gly	Gly	Thr	Ala ₃₆₀	Ala	Thr	Gly	Ala	Cys ₃₆₅	Ala	Ala	Gly
Cys	Gly ₃₇₀	Cys	Cys	Cys	Ala	Gly ₃₇₅	Ala	Thr	Ala	Ala	Cys ₃₈₀	Ala	Ala	Thr	Gly
Gly ₃₈₅	Gly	Cys	Ala	Thr	Gly ₃₉₀	Cys	Cys	Thr	Thr	Ala ₃₉₅	Thr	Gly	Cys	Cys	Gly ₄₀₀
Thr	Gly	Ala	Cys	Cys ₄₀₅	Gly	Ala	Cys	Gly	Cys ₄₁₀	Cys	Gly	Thr	Thr	Cys ₄₁₅	Thr
Gly	Gly	Cys	Thr ₄₂₀	Cys	Cys	Thr	Cys	Ala ₄₂₅	Thr	Gly	Thr	Cys	Gly ₄₃₀	Gly	Gly
Gly	Gly	Gly ₄₃₅	Gly	Ala	Gly	Gly	Cys ₄₄₀	Thr	Gly	Gly	Gly	Ala ₄₄₅	Gly	Thr	Thr
Cys	Ala ₄₅₀	Cys	Ala	Thr	Gly	Cys ₄₅₅	Cys	Cys	Cys	Gly	Cys ₄₆₀	Cys	Cys	Cys	Cys
Gly ₄₆₅	Gly	Cys	Cys	Cys	Thr ₄₇₀	Cys	Ala	Cys	Cys	Cys ₄₇₅	Thr	Cys	Ala	Thr	Cys ₄₈₀

sequence listing_ST25.txt

Thr Thr Cys Gly Ala Cys Cys Gly Cys Cys Ala Thr Cys Cys Cys Ala
485 490 495

Thr Cys Gly Cys Cys Gly Cys Cys Cys Thr Cys Cys Thr Gly Thr Gly
500 505 510

Cys Thr Ala Cys Cys Cys Gly Gly Cys Cys Gly Cys Gly Cys Gly Ala
515 520 525

Thr Ala Cys Cys Thr Thr Ala Thr Gly Gly Gly Cys Ala Gly Cys Ala
530 535 540

Thr Gly Ala Cys Cys Cys Cys Cys Cys Ala Gly Gly Cys Cys Gly Thr
545 550 555 560

Gly Cys Thr Gly Gly Cys Gly Thr Thr Cys Gly Thr Gly Gly Cys Cys
565 570 575

Cys Thr Cys Ala Thr Cys Cys Cys Gly Cys Cys Gly Ala Cys Cys Thr
580 585 590

Thr Gly Cys Cys Cys Gly Gly Cys Ala Cys Ala Ala Ala Cys Ala Thr
595 600 605

Cys Gly Thr Gly Thr Thr Gly Gly Gly Gly Gly Cys Cys Cys Thr Thr
610 615 620

Cys Cys Gly Gly Ala Gly Gly Ala Cys Ala Gly Ala Cys Ala Cys Ala
625 630 635 640

Thr Cys Gly Ala Cys Cys Gly Cys Cys Thr Gly Gly Cys Cys Ala Ala
645 650 655

Ala Cys Gly Cys Cys Ala Gly Cys Gly Cys Cys Cys Cys Gly Gly Cys
660 665 670

Gly Ala Gly Cys Gly Gly Cys Thr Thr Gly Ala Cys Cys Thr Gly Gly
675 680 685

Cys Thr Ala Thr Gly Cys Thr Gly Gly Cys Cys Gly Cys Gly Ala Thr
690 695 700

Thr Cys Gly Cys Cys Gly Cys Gly Thr Thr Thr Ala Cys Gly Gly Gly
705 710 715 720

Cys Thr Gly Cys Thr Thr Gly Cys Cys Ala Ala Thr Ala Cys Gly Gly
725 730 735

sequence listing_ST25.txt

Thr Gly Cys Gly Gly Thr Ala Thr Cys Thr Gly Cys Ala Gly Gly Gly
740 745 750

Cys Gly Gly Cys Gly Gly Gly Thr Cys Gly Thr Gly Gly Thr Gly Gly
755 760 765

Gly Ala Gly Gly Ala Thr Thr Gly Gly Gly Gly Ala Cys Ala Gly Cys
770 775 780

Thr Thr Thr Cys Gly Gly Gly Gly Ala Cys Gly Gly Cys Cys Gly Thr
785 790 795 800

Gly Cys Cys Gly Cys Cys Cys Cys Ala Gly Gly Gly Thr Gly Cys Cys
805 810 815

Gly Ala Gly Cys Cys Cys Cys Ala Gly Ala Gly Cys Ala Ala Cys Gly
820 825 830

Cys Gly Gly Gly Cys Cys Cys Ala Cys Gly Ala Cys Cys Cys Cys Ala
835 840 845

Thr Ala Thr Cys Gly Gly Gly Gly Ala Cys Ala Cys Gly Thr Thr Ala
850 855 860

Thr Thr Thr Ala Cys Cys Cys Thr Gly Thr Thr Thr Cys Gly Gly Gly
865 870 875 880

Cys Cys Cys Cys Cys Gly Ala Gly Thr Thr Gly Cys Thr Gly Gly Cys
885 890 895

Cys Cys Cys Cys Ala Ala Cys Gly Gly Cys Gly Ala Cys Cys Thr Gly
900 905 910

Thr Ala Thr Ala Ala Cys Gly Thr Gly Thr Thr Thr Gly Cys Cys Thr
915 920 925

Gly Gly Gly Cys Cys Thr Thr Gly Gly Ala Cys Gly Thr Cys Thr Thr
930 935 940

Gly Gly Cys Cys Ala Ala Ala Cys Gly Cys Cys Thr Cys Cys Gly Thr
945 950 955 960

Cys Cys Cys Ala Thr Gly Cys Ala Cys Gly Thr Cys Thr Thr Thr Ala
965 970 975

Thr Cys Cys Thr Gly Gly Ala Thr Thr Ala Cys Gly Ala Cys Cys Ala
980 985 990

sequence listing_ST25.txt

Ala Thr Cys Gly Cys Cys Cys Gly Cys Cys Gly Gly Cys Thr Gly Cys
 995 1000 1005

Cys Gly Gly Gly Ala Cys Gly Cys Cys Cys Thr Gly Cys Thr Gly
 1010 1015 1020

Cys Ala Ala Cys Thr Thr Ala Cys Cys Thr Cys Cys Gly Gly Gly
 1025 1030 1035

Ala Thr Gly Gly Thr Cys Cys Ala Gly Ala Cys Cys Cys Ala Cys
 1040 1045 1050

Gly Thr Cys Ala Cys Cys Ala Cys Cys Cys Cys Ala Gly Gly Cys
 1055 1060 1065

Thr Cys Cys Ala Thr Ala Cys Cys Gly Ala Cys Gly Ala Thr Cys
 1070 1075 1080

Thr Gly Cys Gly Ala Cys Cys Thr Gly Gly Cys Gly Cys Gly Cys
 1085 1090 1095

Ala Cys Gly Thr Thr Thr Gly Cys Cys Cys Gly Gly Gly Ala Gly
 1100 1105 1110

Ala Thr Gly Gly Gly Gly Gly Ala Gly Gly Cys Thr Ala Ala Cys
 1115 1120 1125

<210> 177
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-3

<400> 177
 atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttcgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcccggagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc ccacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
 atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggtg ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
accaacatcg tgcttggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct ggacctggct atgctggctg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggg cgtggcgggg ggactgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttgccaa acgcctccgt	960
tccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgcctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080
atatgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 178

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-4

<400> 178

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgatc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttgccaa acgcctccgt	960

sequence listing_ST25.txt

```

cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcgccg gagatggggg aggctaac 1128

```

```

<210> 179
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-5

```

```

<400> 179
atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgaccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ttcggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggtt tgacctggt atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc 900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcgccg gagatggggg aggctaac 1128

```

```

<210> 180
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-6

```

sequence listing_ST25.txt

```

<400> 180
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc      540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc      600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgcttgg gccttgagc tcttgccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

```

<210> 181
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-7

```

```

<400> 181
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct      420

```

sequence listing_ST25.txt

cctcatatcg	ggggggagggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccgcc	atcccatcgc	cgccctcctg	tgctacccgg	ccgcgcgata	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcgttc	gtggccctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttccggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gcgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctgcttgcca	atacggtgcg	gtatctgcag	ggcggcgggg	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggccgt	gccgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggacac	gttatttacc	ctgtttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtataacgt	gtttgcctgg	gccttgagcg	tcttgcccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgcccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctaac		1128

<210> 182

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-8

<400> 182

atggcttcgt	acccttgcca	tcaacacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	agcaagaagc	cacggaagtc	120
cgcctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctgggtt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcagggtg	ctgggggctt	ccgagacaat	cgcgaaacatc	300
tacaccacac	aacaccgcct	cgaccagggt	gagatatcgg	ccggggatgc	ggcggtggtg	360
atgacaagcg	cccagataac	aatgggcatg	ccttatgccg	tgaccgacgc	cgttctggct	420
cctcatatcg	ggggggagggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccgcc	atcccatcgc	cgccctcctg	tgctacccgg	ccgcgcgata	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcgttc	gtggccctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttccggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gcgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctgcttgcca	atacggtgcg	gtatctgcag	ggcggcgggg	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggccgt	gccgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840

sequence listing_ST25.txt

```

cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttggccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccc ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 183
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase) sequence-9

```

```

<400> 183
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccataaca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgctggagc agaaaatgcc cacgtactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggatgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ccttatgccg taaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcgctt ttggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggt cgtggcgga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttggacg tcttggccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccc ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 184
<211> 1128
<212> DNA
<213> artificial sequence

```

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-10

<400> 184

```
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccacccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccag acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128
```

<210> 185

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-11

<400> 185

```
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
```


sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccagag gacaaacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgtca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttattttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 186
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-12

<400> 186	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcacc	900
aacggcgacc tgtataacgt gtttgcttg gccttgacg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gttgcccgg gagatggggg aggctaac	1128

<210> 187
 <211> 1128
 <212> DNA
 <213> artificial sequence
 <220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-13

<400> 187

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtgta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgacc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca ttgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgacg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg	1080

atctgcgacc tggcgcgcac gtttggccgg gagatggggg aggctaac 1128

<210> 188
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-14

<400> 188
 atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc 540
 agcatgacct cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tgttgggggc ctttcggag gagagacaca ttgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc 900
 aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgggcaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttggccgg gagatggggg aggctaac 1128

<210> 189
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-15

<400> 189
 atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctt tgctaccggc ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ccttccggag gacagacaca ttgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgcctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

```

<210> 190
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-16

```

```

<400> 190
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctaccg	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctcctg	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gtttggccg gagatggggg aggctaac	1128

<210> 191
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-17

<400> 191	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttcgc cctcgccggc agcaagaagc cacggaagtc	120
cgcttggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccg	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcggaacca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc tgtataacgt gtttgccctgg gccttgagacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 192
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-18

<400> 192	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tctcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccctt caccctcatc	480
tctgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag gttgccgagc cccagagcaa cgcggaccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctgg gccttgagacg tcttgcccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 193
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence_listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-19

<400> 193

```
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacgggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct catcctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctagccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggc cgtggcgggg ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgggcaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128
```

<210> 194

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-20

<400> 194

```
atggcttcgt atccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacgggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
```

sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccaccc aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcgggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac	1128

<210> 195

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-21

<400> 195

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660


```

sequence_listing_ST25.txt
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttggtcaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

```

<210> 196
<211> 1128
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-22

```

```

<400> 196
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggta ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc 540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tggtgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttggtcaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080

```

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 197
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-23

<400> 197
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcggtgcgc cctcgccggc agcaagaagc cacggaagtc 120
 cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccctt caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc 540
 agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgcctcg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
 aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caagcgcctg ccggctgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 198
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-24

<400> 198
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgt 60

sequence listing_ST25.txt

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gttggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgcgccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccc cggtctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac	1128

<210> 199

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-25

<400> 199

atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg ccccgaggtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 200
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-26

<400> 200	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcttgagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggt ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct cgccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgaggtt gctggccccc	900

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 201
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-27

<400> 201	
atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cggccggagc agaaaatgcc cacgtactg cgggtttata tagacgggcc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg ccagataaac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggtc tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggc cgtggcgga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccagggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 202
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-28

<400> 202

```

atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cggaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg cttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata cttatgggc      540
agcatgaccc cccaggccgt gttggcggtc gtggccctca tccgcccac cttgcccggc      600
acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccagtt gctggcccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                    1128

```

<210> 203

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-29

<400> 203

```

atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

```

sequence_listing_ST25.txt

gtacccgagc cgatgactta ctggcggggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgacccccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 204

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-30

<400> 204

atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggccc ccacgggatg	180
gggaaaacca ccaccacgca actgctgggt gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence_listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgacctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 205

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-31

<400> 205

atggcttcgt acccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcccgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcgggtggt	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag gccggcgggt cgtggcggca ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgacctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaaggctc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 206
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-32

<400> 206
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cggaacatc 300
 tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
 agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttggccggc 600
 acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
 aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 207
 <211> 1131
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-33

<400> 207
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggagggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc 540
agcatgacc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgcggcg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccattgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctcc ataccgacga 1080
tctgcgacct ggcgcgcacg tttgccggg agatggggga ggctaactga a 1131

```

```

<210> 208
<211> 1131
<212> DNA
<213> artificial sequence

```

```

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-34

```

```

<400> 208
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcaaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggagggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc ccaggccgtg ctggcggttc tgggccctcat cccgccgacc ttgcccggca	600
caaacatcgt gttggggggc cttccggagg acagacacat cgaccgcctg gccaaacgcc	660
agcgccccgg cgagcggctt gacctggcta tgctggccgc gattcgccgc gtttacgggc	720
tgcttgccaa tacggtgcgg tatctgcagg gcggcgggtc gtggcgggag gattggggac	780
agctttcggg gacggccgtg ccgccccagg gtgccgagcc ccagagcaac gcgggcccac	840
gaccccatat cggggacacg ttattttacc tgtttcgggc ccccgagttg ctggccccca	900
acggcgacct gtataacgtg tttgcctggg ccttgacgt cttggccaaa cgcctccgtc	960
ccatgcacgt ctttatcctg gattacgacc aatcgcccgc cggctgccgg gacgccctgc	1020
tgcaacttac ctccgggatg gtccagaccc acgtcaccac cccaggctcc ataccgacga	1080
tctgcgacct ggcgcgcacg tttggccggg agatggggga ggctaactga a	1131

<210> 209

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-35

<400> 209

atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata taaacggctc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg cgggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc	tgtataacgt	gtttgcctgg	gccttggacg	tcttggccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctaac		1128

<210> 210
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-36

<400> 210	
atggcttcgt	acccctgcc
tcaacacgcg	tctgcgttcg
accaggctgc	gcgttctcgc
60	
ggccatagca	accgacgtac
ggcgttgccg	cctcgccggc
agcaagaagc	cacggaagtc
120	
cgcctggagc	agaaaatgcc
cacgctactg	cgggtttata
tagacggtcc	tcacgggatg
180	
gggaaaacca	ccaacacgca
actgctggtg	gccctggggt
cgcgcgacga	tatcgtctac
240	
gtacccgagc	cgatgactta
ctggcagggt	ctgggggctt
ccgagacaat	cgcgaaacatc
300	
tacaccacac	aacaccgcct
cgaccagggt	gagatatcgg
ccggggacgc	ggcgggtggt
360	
atgacaagcg	cccagataac
aatgggcatg	ccttatgccg
tgaccgacgc	cgttctggct
420	
cctcatatcg	ggggggaggc
tgggagctca	catgccccgc
ccccggccct	caccctcatc
480	
tctgaccgcc	atcccatcgc
cgccctcctg	tgctaccggg
ccgcgcgata	ccttatgggc
540	
agcatgaccc	cccaggccgt
gctggcggtc	gtggccctca
tcccgccgac	cttgcccggc
600	
acaaacatcg	tggtgggggc
ccttccggag	gacagacaca
tcgaccgcct	ggccaaacgc
660	
cagcgccccg	gcgagcggct
tgacctggct	atgctggccg
cgattcgccg	cgtttacggg
720	
ctgcttgcca	atacgggtgcg
gtatctgcag	ggcggcgggg
cgtggcgggg	ggattggggg
780	
cagctttcgg	ggacggccgt
gccgccccag	ggtgccgagc
cccagagcaa	cgcgggcccc
840	
cgaccccata	tcggggacac
gttatttacc	ctgtttcggg
cccccgagtt	gctggcccc
900	
aacggcgacc	tgtataacgt
gtttgcctgg	gccttggacg
tcttggccaa	acgcctccgt
960	
cccatgcacg	tctttatcct
ggattacgac	caatcgcccc
ccggctgccg	ggacgccctg
1020	
ctgcaactta	cctccgggat
ggtccagacc	cacgtcacca
ccccaggctc	cataccgacg
1080	
atctgcgacc	tggcgcgcac
gtttgcccgg	gagatggggg
aggctaac	
1128	

<210> 211
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-37

<400> 211

```
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagt cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgacct cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acáaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128
```

<210> 212

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-38

<400> 212

```
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
```

sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac	1128

<210> 213
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-39

<400> 213	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgccctgc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence_listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 214
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-40

<400> 214	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atatggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 215
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-41

<400> 215
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cggttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc 540
agcatgacct cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ccttcgagag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgagg ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggacat gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 216
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-42

<400> 216
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgccctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggagggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
acaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgcgccg gcgagcggtt tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggtt cgtggcgggg ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctaccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtacca cccaggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

<210> 217
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-43

```

<400> 217
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccaggtt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggagggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgac gttgcccgg gagatggggg aggctaac	1128

<210> 218
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-44

<400> 218	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgctggagc agaaaatgcc cagctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc tgtataacgt gtttgacctg gccttgagcg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080
atctgcgacc tggcgcgac gtttgcccg ggagtggggg aggctaac	1128

<210> 219
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-45

<400> 219	
atggcttcgt acccctgcc tcaacacg cg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cggccggagc agaaaatgcc cacgtactg cgggtttata tagacggtcc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg ccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcggta ccttatgggc	540
agcatgacc ccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggt tgacctggct atgctggcg cgattcgccg cgtttacggg	720
ctacttgcca atacggtcg gtatctgcag tgcggcggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc ccagagcaa cgcgggcca	840
cgacccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgacctg gccttgagcg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggtc cataccgacg	1080
atctgcgacc tggcgcgac gtttgcccg gagatggggg aggctcac	1128

<210> 220
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-46

<400> 220

```

atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg tgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta      360
atgacaagcg ccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcgata ccttatgggc      540
agcatgaccc ccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg      720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc ccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc      900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttggccaa acgcctccgt      960
cccattgcacg tctttatcct ggattacgac caatcgcccc cggttgccg ggacgccctg     1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128

```

<210> 221

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-47

<400> 221

```

atggcttcgt acccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240

```

sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggtg ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgacg tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggtcac	1128

<210> 222
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-48

<400> 222	
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc	120
cgcttgagc agaaaatgcc cagctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgttacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtgccc ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 223
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-49

<400> 223	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc aacaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccgg ccgtgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtgccc ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc cggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 224
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-50

<400> 224
 atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgccg cctcgccggc aacaagaagc cacggaagtc 120
 cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
 gtacccgagc cgataactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc 480
 ttcgaccggc atcccatcgc cgccctcctg tgttaccggc ccgcgcgata ctttatgggc 540
 agcatgacct cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tggtgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
 aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccg ggacgccctg 1020
 ctgcaactta cctccgggat ggtccagacc cacgtacca ccccggtc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 225
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-51

<400> 225
 atggcttcgt acccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtc gtggtcctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggccccc 900
aacggcgacc tgtacaacgt gtttgcttg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

<210> 226
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-52

```

<400> 226
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac 240
gtaccaagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```


sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 227
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-53

<400> 227	
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cagcgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtaccaagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca ccccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 228
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-54

<400> 228	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgt gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc	120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcggggt ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aaccccgct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccgg ccgcgcgata ccttatgggc	540
agcatgacct cccaggccgt gctggcggtt gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgcttggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggctg cgattcgccg cgtttacgag	720
ctacttgcca atacggtgcg gtatctgcag ggcggcggt cgtggcggga ggactgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca ccccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg cggctaac	1128

<210> 229
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-55

<400> 229

atggcttcgt	acccctgcca	tcaacacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	aacaagaagc	cacggaagtc	120
cgcctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctggggt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcgggtg	ctgggggctt	ccgagacaat	cgcgaaacatc	300
tacaccacac	aacaccgcct	cgaccagggt	gagatatcgg	ccggggacgc	ggcgggtggt	360
atgacaagcg	cccagataac	aatgggcatg	ccttatgccg	tgaccgacgc	cgttctggct	420
cctcatatcg	ggggggaggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccgcc	atcccatcgc	cgccctcctg	tgttacccgg	ccgcgcgata	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcggtc	gtggccctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgcttggggc	ccttcgggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gcgagcggct	tgacctggct	atgctggctg	cgattcgccg	cgtttacggg	720
ctacttgcca	atacggtgcg	gtatctgcag	tgcggcgggt	cgtggcgggg	ggactgggga	780
cagcttttcg	ggacggccgt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggaaac	gttatttacc	ctgtttcggg	cccccgagtt	gctggcccc	900
aacggcgacc	tgtacaacgt	gtttgcctgg	gccttgagc	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccc	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	catgtcacca	ccccaggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccgg	gagatggggg	aggctcac		1128

<210> 230

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-56

<400> 230

atggcttcgt	accccgcca	ttagcacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	agcaagaagc	cacggaagtc	120
cggccggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	ccacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctggggt	cgcgcgacga	tatcgtctac	240

sequence_listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccaca tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 231

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-57

<400> 231

atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggta ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg	gtgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctacttgcca	atacggtgcg	gtatctgcag	tgcggcgggt	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggcctt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggaaac	gttatttacc	ctgtttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtacaacgt	gtttgcctgg	gccttgagc	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccg	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccggctc	cataccgacg	1080
atctgcgacc	tggcgcgcac	gtttgcccg	gagatggggg	aggctaac		1128

<210> 232

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-58

<400> 232

atggcttcgt	accccgcca	tcaacacgcg	tctgcgttcg	accaggctgc	gcgttctcgc	60
ggccatagca	accgacgtac	ggcgttgcg	cctcgccggc	agcaagaagc	cacggaagtc	120
cacctggagc	agaaaatgcc	cacgctactg	cgggtttata	tagacggtcc	tcacgggatg	180
gggaaaacca	ccaccacgca	actgctggtg	gccctgggtt	cgcgcgacga	tatcgtctac	240
gtacccgagc	cgatgactta	ctggcgggtg	ctgggggctt	ccgagacaat	cgcgaaacatc	300
tacaccacac	aacaccgcct	cgaccagggt	gagatatcgg	ccggggacgc	ggcgggtggt	360
atgacaagcg	cccagataac	aatgggcatg	ccttatgccg	tgaccgacgc	cgttctggct	420
cctcatatcg	ggggggaggc	tgggagctca	catgccccgc	ccccggccct	caccctcatc	480
ttcgaccacc	atcccatcgc	cgccctcctg	tgctaccccg	ccgcgcggta	ccttatgggc	540
agcatgaccc	cccaggccgt	gctggcgctt	gtggtcctca	tcccgccgac	cttgcccggc	600
acaaacatcg	tgttgggggc	ccttcgggag	gacagacaca	tcgaccgcct	ggccaaacgc	660
cagcgccccg	gtgagcggct	tgacctggct	atgctggccg	cgattcgccg	cgtttacggg	720
ctacttgcca	atacggtgcg	gtatctgcag	tgcggcgggt	cgtggcggga	ggattgggga	780
cagctttcgg	ggacggcctt	gacgccccag	ggtgccgagc	cccagagcaa	cgcgggccca	840
cgaccccata	tcggggaaac	gttatttacc	ctgtttcggg	cccccgagtt	gctggccccc	900
aacggcgacc	tgtacaacgt	gtttgcctgg	gccttgagc	tcttgccaa	acgcctccgt	960
cccatgcacg	tctttatcct	ggattacgac	caatcgcccg	ccggctgccg	ggacgccctg	1020
ctgcaactta	cctccgggat	ggtccagacc	cacgtcacca	ccccggctc	cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 233
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-59

<400> 233
 atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc 60
 ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
 cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
 gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
 gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc 300
 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
 atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
 cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
 ttcgaccgcc atcccatcgc cgccctcctg tgctaccgg ccgcgcgata ctttatgggc 540
 agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc 600
 acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
 cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
 ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcgggg ggattgggga 780
 cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca 840
 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccagatt gctggcccc 900
 aacggcgacc tgtacaacgt gtttgctgg gccttggaag tcttgggcaa acgcctccgt 960
 cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgcctg 1020
 ctgcaactta cctccgggat gatccagacc cacgtcacca cccaggctc cataccgacg 1080
 atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

<210> 234
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-60

<400> 234
 atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgttaccggc ccgcgcgata ccttatgggc 540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca ccgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggtc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaac 1128

```

<210> 235
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-61

```

<400> 235
atggcttcgt acccctgcc tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc aacaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgttacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctgggtgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca ccgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacgag	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 236

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-62

<400> 236

atggcttcgt accccggcca tcagcacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cacccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc	900

sequence listing_ST25.txt

aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccaggttc cataccgacg	1080
atctgcgacc tggcgcgac gtttgcccgg gagatggggg aggctcac	1128

<210> 237
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-63

<400> 237	
atggcttcgt acccggcca tcaacacg cg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgtactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc cccggccct caccctcatc	480
ttcgaccgcc atcccatcg cgccctcctg tgctaccgg ccgcgcggtg ccttatgggc	540
agcatgaccc cccaggccgt gctggcgctt gtggtcctca tccgcgcgac cttgcccggc	600
acaaacatcg tggtgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gttggcccc	900
aacggcgacc tgtacaacgt gtttgccctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggttc cataccgacg	1080
atctgcgacc tggcgcgac gtttgcccgg gagatggggg aggctcac	1128

<210> 238
 <211> 1128
 <212> DNA
 <213> artificial sequence

sequence listing_ST25.txt

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-64

<400> 238

```
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacgggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
gtacccgagc cgatgactta ctggcggggt ctgggggctt ccgagacaat cggaacatc      300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg      360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct      420
cctcatatcg ggggggaggg tgggagctca catgccccgc cccggccct caccctcatc      480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggta ccttatgggc      540
agcatgaccc cccaggccgt gctggcggtc gtggtcctca tcccgccgac cttgcccggc      600
acaacatcg tgttgggggc ctttcgggag gacagacaca tcgaccgcct ggccaaacgc      660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg ccgttacggg      720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga      780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca      840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggccccc      900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttggccaa acgcctccgt      960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggtgccg ggacgccctg     1020
ctgcaactta cctccgggat gatccagacc cacgtcacca cccaggctc cataccgacg     1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac                     1128
```

<210> 239

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-65

<400> 239

```
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc      60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc      120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacgggtcc tcacgggatg      180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac      240
```

sequence listing_ST25.txt

gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggta ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaatgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggccccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac	1128

<210> 240
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-66

<400> 240	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc	120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggg gagatatcgg ccgggggacgc ggcggtggta	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggg tgggagctca catgccccgc ccccggccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ccttatgggc	540
agcatgaccc cccaggccgt gctggcgttc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ccttccggag gacagacaca tcgaccgcct ggccaaacgc	660

sequence listing_ST25.txt

cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggt cgtggcggga ggattgggga	780
cagcttttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtataacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg	1080
atctgcgacc tgggtgcgcac gtttgcccgg gagatggggg aggctaac	1128

<210> 241
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-67

<400> 241	
atggcttcgt acccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atccaatcgc cgccctcctg tgctaccgg ccgcgcggta ccttatgggc	540
agcatgacct cccaggccgt gctggcgctt gtggtcctca tcccgccgac cttgcccggc	600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga	780
cagcttttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggcccc	840
cgaccccata tcgggggaaac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080

sequence listing_ST25.txt

atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac 1128

<210> 242
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-68

<400> 242
atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cacctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcggggtg ctgggggctt ccgagacaat cgcgaaacatc 300
tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ccttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atccaatcgc cgccctcctg tgctaccgg ccgcgcggta ccttatgggc 540
agcatgacct cccaggccgt gctggcggtt gtggtcctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc ctttcggag gacagacaca tcgaccacct ggccaaacgc 660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggt cgtggcggga ggattgggga 780
cagctttcgg ggacggcctt gacgccccag ggtgccgagc cccagagcaa cgcgggccca 840
cgaccccata tcggggaaac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtacaacgt gtttgctgg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctcac 1128

<210> 243
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-69

<400> 243
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60

sequence listing_ST25.txt

```

ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcctggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatggacatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480
ttcgaccgcc atcccatcgc cgccctcctg tgctaccggy ccgcgcgata ctttatgggc 540
agcatgacc cccaggccgt gctggcgctt gtggccctca tcccgccgac cttgcccggc 600
acaaacatcg tgttgggggc cttccggag gacagacaca tcgaccgcct ggccaaacgc 660
cagcgccccg gcgagcggtt tgacctggct atgctggccg cgattcgccg cgtttacggg 720
ctgcttgcca atacggtgcg gtatctgcag ggcggcggtt cgtggcgggg ggattgggga 780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggcccc 840
cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
aacggcgacc tgtataacgt gtttgcttgg gccttgagc tcttgccaa acgcctccgt 960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg 1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca cccaggctc cataccgacg 1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac 1128

```

<210> 244

<211> 1128

<212> DNA

<213> artificial sequence

<220>

<223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
sequence-70

<400> 244

```

atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc 60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc 120
cgcccggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc ccacgggatg 180
gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
gtacccgagc cgatgactta ctggcgggtg ctgggggctt ccgagacaat cgcgaacatc 300
tacaccacac aacaccgcct cgaccaggtg gagatatcgg ccggggacgc ggcggtggta 360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct 420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc 480

```

sequence_listing_ST25.txt

ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcggta ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggctctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gtgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctacttgcca atacggtgcg gtatctgcag tgcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccct gacgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccccata tcggggaaac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900
aacggcgacc tgtacaacgt gtttgccctg gccttgagc tcttgccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgccc cggtctgcc ggacgcctg	1020
ctgcaactta cctccgggat ggtccagacc catgtcacca cccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gttgcccgg gagatggggg aggtcac	1128

<210> 245
 <211> 1128
 <212> DNA
 <213> artificial sequence

<220>
 <223> HSV1-tk (herpes simplex virus type-1 thymidine kinase)
 sequence-71

<400> 245	
atggcttcgt acccctgcca tcaacacgcg tctgcgttcg accaggctgc gcgttctcgc	60
ggccatagca accgacgtac ggcgttgcg cctcgccggc agcaagaagc cacggaagtc	120
cgcttggagc agaaaatgcc cacgctactg cgggtttata tagacggtcc tcgcgggatg	180
gggaaaacca ccaccacgca actgctggtg gccctggggt cgcgcgacga tatcgtctac	240
gtacccgagc cgatgactta ctggcaggtg ctgggggctt ccgagacaat cgcgaaacatc	300
tacaccacac aacaccgcct cgaccagggt gagatatcg cgggggacgc ggcggtggtg	360
atgacaagcg cccagataac aatgggcatg ctttatgccg tgaccgacgc cgttctggct	420
cctcatatcg ggggggaggc tgggagctca catgccccgc ccccgccct caccctcatc	480
ttcgaccgcc atcccatcgc cgccctcctg tgctacccgg ccgcgcgata ctttatgggc	540
agcatgaccc cccaggccgt gctggcggtc gtggccctca tcccgccgac cttgcccggc	600
acaaacatcg tggtgggggc ctttccggag gacagacaca tcgaccgcct ggccaaacgc	660
cagcgccccg gcgagcggct tgacctggct atgctggccg cgattcgccg cgtttacggg	720
ctgcttgcca atacggtgcg gtatctgcag ggcggcgggg cgtggcgggg ggattgggga	780
cagctttcgg ggacggccgt gccgccccag ggtgccgagc cccagagcaa cgcgggccca	840
cgacccccata tcgggggacac gttatttacc ctgtttcggg cccccgagtt gctggcccc	900

sequence listing_ST25.txt

aacggcgacc tgtataacgt gtttgcctgg gccttggacg tcttggccaa acgcctccgt	960
cccatgcacg tctttatcct ggattacgac caatcgcccg ccggctgccg ggacgccctg	1020
ctgcaactta cctccgggat ggtccagacc cacgtcacca ccccaggctc cataccgacg	1080
atctgcgacc tggcgcgcac gtttgcccgg gagatggggg aggctaac	1128